

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGACAGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC
 TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
 TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
 CTTTTCTCTTTAAATGAGAAGGCCACCAATGTCCCTTCGTGCTATTGCTACTGGTACCG
 TCATTATTCCTTTGGGCACCTTTGGTTGTTTGTACCTGCCGAGCTTCCTGCATGGATGCTA
 AAAGTGTATGCAATGTTTCTGACTCTCGTTTTTGGTCGAAGTGGTGGTGGCATCGTAGG
 ATTTGTTTTAGACATGAGATTAAGAAGAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
 AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
 TGTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAGGATT
 TCCTAAGAGTTGCTGTAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
 ATGAAGGTTGTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
 ATTCCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTCTCGCCTACTGCCWCTCTCG
 TGCCATAACAAATAACAGTATGAGATAGTGA**TA**CCCAATGTATCTGTGGGCTTATTCCTCT
 CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAAGTTGCTTGGCTGGAGAACTG
 ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
 GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
 TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCATGTTAGATCG
 TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNENYFSLLEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNTNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCGGTCTCTCGGACCTGTCAAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCGACCGCGTGTCTGAGCCCTGGGCACGCGGAACGGGAGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGACTGGG
 GCCGGGTAGGCTCTGGAAAGGGCCCGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAAAGAGGT
 GTTCCCTCTTTGGGGGTCTCTACCAGAAAGGTTCTTGGGGGTGCGCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTAGTTGTTAAAAACAAATAGGATGCAAATTC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAAACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCAACAGCAACAGGCCGAGAACAGTG
 CAGTACCACTGCTGACACAAGGAGCCAACCACGGGACCTGTTTCGGCCCAAGGAGGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAATATCTGACTCAGGGTACCTCCAGTGGAAT
 GAAAAGTGTTCTGCCCAGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAAATGCTCCGCTGATGGCAGAGTAA
 TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
 TGAGCAGAAAACACGATAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRFPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAAATGTGGGTGACCTTCGTCTCAGGCTTCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCCTACCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

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GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNAWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCATTCTGCAGTGGAAATTTTCATGAAGTAGCAAGAGGACACCATCTT
 CTTGTATTATACAAGAAAGGAGTGTAACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTTTACTGGAATGTGACTCGGGCTTTGGAACTTGGCAGCC
 AGAATCTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
 CTGATCAATAATGCTGGTGTCCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA
 ATCGTTGGAGGGGGCTATACCTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
 GACATCAAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTATGTGTGAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
 TTCAAGAACACATCTCCTTTTCAACCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA
 TCGTGCTTATTTGGATTGCAAAAGGAGTCCACCATCGCTGGTGGTATCCAGGGTCCCTG
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 ATTTAGGCTTTGCTGCTTGTGTGATGTAAGGGAAATTGAAAGACTTGGCCATTCAAATG
 ATCTTTACCGTGGCTGCCCATGCTTATGGTCCCCAGCATTACAGTAACTGTGTAATGTT
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 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
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ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSIEPGLFKTNLADPVKVIKKLAIWQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCGC**ATG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTTACGCCCGCAGTGGGCGGGGCCCCCTTGGGCGCGTCCGCCACCACT
 GTAGTCATGTACCCACCGCCGCCCGCGCCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGCGCGCTCGTGCTGGAGGAAATGGA
 AGCAACTGTGAGATTGACAGCGGAATATGATTCTCTTCTCTCTTGGCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAAGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTTAAAACAGCAAAATCCACCGCTCTTACCAG
 CTCCTTCAGAAGGCGGACACCGACCTGAGAACTTACCTGAGATTTCTGTCACAGAAGACAAA
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 CTCCTTCAAGAAGAGCAGAAGTGCCCAAGCCCTCCCCTGCCACCGGCCAGGACACAGGG
 CACACCATGTCATCTGAACATATGCCAGAAGGGCGTGATTGACGCTCTTCTGTCATGTCATGGA
 AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT
 GAGTGGTTTGGCGCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAAGGAGC
 TGGAGCTCAACCTCTTTGAGAGCAGATCCGCTACTCTGGGGGGCTCTGAGTGCCCTACCAC
 CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCTTGC
 CTTTCAAGAACCACTCCAGGATTCTTACTCGGATGTGAACATCGGACTGGAGTTGCCACC
 CGCCACGCTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTGAGCTGGAGTTCGGG
 GAGCTCTCCGCTCTCAGGGGATAAGAAGTTTTCAGGAGGCAAGTGGAGAAGGTGACACAGCA
 CATCCACGGCCTGTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTCACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
 AGCCATCGAGGGTGTGAGAAGCACTGCTGCGGCCTCCGAGGCCAGTAAGCTCACCTTTG
 TGGGGGAGCTTGCCACGGCCGCTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTCGCCA
 GGGACGCTGGCTCTGGGCGCTTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCACGGA
 GCTCATGGAGACTTGTACAGATGAACCGGAGATGGAGACGGGGCTGAGTCCCGAGATCG
 TGCACCTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGCTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCGGCCAGAGACCGTGAGAGCCTGTTTACCTGTACCGCCTCACAGGGGA
 CCGCAATACAGGACTGGGGCTGGGAGATTTCAGAGCTTCAGCCGATTCACACGGGTCC
 CTGGGGTGGCT**TAG**GGTGGATGGCTGCTGGTGGGGACTTCGGGTGGGCGAGGGAACCTTG
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 CTGAACCTGGCTCTGGGCTCTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
 GGCGCTCAGCTCTGGTGTGATCGGGGTGGGCTGGGCGCTGGAGCCTCCGCTGCTTCTCT
 CAGAAGACAGCAATCATGACTCAGGATTGCTGAAGCCTGAGCAGGCTCTCTGTGGGCGGACCA
 GAGGGGGCTTGCAGGTGGTCCCTGGTACTGGGTGACCGAGTGACAGCCAGGCTGCAGC
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 CTCAGAGGCTCTGAGGCTCAGGGCTGGCTGTGGTGTTCACAGCTGGACTCAGGAGTCTCT
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 CCAGTGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTGCTCTAACCGCAA

FIGURE 10

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
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SKSWRRRCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLSEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTOEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTPELPSRRAEVPTKPPPLPPARTQGTTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSEWFGGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVVDNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAAHPPRWTS DSTVAEVT SIQLEFRELSRLTGDKKFQEA VEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTL GARADSYEYLLKQW IQGGKQETQLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCF LPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSP EIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSF SRFTRVP SGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFENTEAHPLPIWTPA

```

Important features of the protein:**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCGCTCTCCACCTGTTCTGTGGC
 CTGCTCTCGTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
 CCGGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCTGCCCCCAGAG
 CCGCCCCCTGAGCAGTGGGAAGAACGCATCCTGGGGCCCCACCGCTGGCAGTGCTGGT
 GCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
 CGGGCAGCGCTCATCAACGTGGGCTTCTTGAGAGCAGCAACAGCAGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCTTGAGGCTGGGC
 CCTTCCACGTGGCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
 ATCCTGCTGCTCTCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
 CTGGGGCCGCGAGGACGACGATTCTACCGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
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 CCTGCACTGTCTCAACATCATGTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTC
 AGCT**GA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
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 GGACCCCCCTGCCTTCTGCTCACCTACTCTGACCTCCTTACGTGCCAGGCTGTGGG
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FIGURE 12

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
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GQQQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVA
SPELHPLYHYKTYVGGILLSSKQHYRLCNGMSNRFWGWGREDDFYYRIKAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCAAGCCCCTTTACCT**ATGCT**:
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGG
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCG
GGGGGATGCG**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGT
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTT.
CCTGTTCATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTT:
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FIGURE 14

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PRGEGEKVGDG
```

Important features:**Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCCGCGCCGGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCCGCGCTGG
 GCCGCGCCGCGCTCCTGCCC GCCGGGCTCCGGGGCGGCCGTAGGCCAGTGCGCCGCCG
 CTCGCCGCCGAGGCCGCCGCCGAGCATGGAGCCACCCGGACGCCGGCGGGGCCGCCGCGCA
 GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGCGCGCG
 GCGCGCGCGCGCGCGCTGCGCCGCCGCTGCAAGCACGATGGGCGGCCGCCGAGGGCTGGC
 AGGGCGCGGGCGGCCGCCGAGGGCAAGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT
 GCCCCAGATACTCTGCCAACCCGACGGTCAACCCTGATTCTGAGTAACAATAAGATATCCG
 AGCTGAGAATGGCTCATTTTCTGGGTTAAGTCTCCTTGAAGATTTGGACCTCCGAAACAAT
 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTATCTCTAAAAAGATTGGATCT
 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTCCAGGACTCACCAATCTGGTTC
 GGCTAAACCTTTTCGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTGGATTCTTCGCG
 TCATTACGGTCTTTTGAATTCAGACTGAGTATCTTTTGTGTACTGTAACATACTGTGGAT
 GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACAGGTTGTTTATCTCTAAGT
 CACTGCAGGCCCAACAGTACAGCGCTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
 GAATTCGCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTGAAGGAGACAGCCT
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 TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTGAGCTGGATCTACTGGAATTTG
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 AGAGTTCTGCACGTAAGTGTCTCCAGAGAGGGTGGTAAACAACAAGGTGACTTCAGATGG
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 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT
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 GAGCTCAGGTTTATTCAACATATTCACCAATATTGCTCTGGAAGCTTATGTCACTCAAGTCT
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 ACTTTCCGATTATGGGAGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT
 GCAATGTTTCAAAATACATTTTTCGAGTCTGGCACTAAAGGTATGTTACATTTGCAATCATTT
 AAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA
 AAAGATTTTTTTTTCGAGGAAGATAGGTATTATTGCTTTTGCTGTTTAAAGAAAATA
 ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT
 CTTACATAAAAAATATCAGAAATTACATTTTATACTGCGAGTGGTATAAATGCAAAATATACT
 ATTGTTACATGTAAGAAATTTTTATTGACTTAAAGTTTATTATTGTTTTTTTGTCTCCT
 GATTTTTAAGACAATAAGATGTTTTCATGGGCCCTAAAGATATCATGAGCCTTTGGCACTGC
 GCTGCCACGCTGCTGGGAAGTCAACCTGAGACAGGTGTTTAAATCAAGCAAGCTGTAT
 ATCAAAATTTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAGTATTCTA
 TTGAAGCAAGCAAAATGAAGCATTTTTTACTGATTTTTTAAAAATGGTGCTTTAGATATATTT
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 TACTTTATTCTGTCTTGTCCCTCAATAATATCACAACAATAATTCAGTCATTTTAATGGC
 TGCATAATAACTGATCAACAGGCTGTAGTGTCTGTTTTAGTTGAGCACTCAATAAATA
 TTGAATGAATGAAGCAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRGRAQFPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSELAQVLPPDTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLASLRSLEFQT
 EYLLCDCNILLWMHRWVEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGC HVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTL AGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQ MPLNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFRGRTKEEKSKELGDMVMDIASNIMLA
 DERVWLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDR TGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYIILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

FIGURE 17

CGTGGGGATGTCTAGGAGCTCGAAGGTGGTGTGGGCCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCC
 CAAGTGTGGCTTAATCCGCTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGACCACCATCACAACCACCACGACGTATCTTCGGG
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTCTGCTTCTCCGTGACCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCTGTCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCGGCGAG
 ATCATCTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCTGCTGAACCTGGGG
 GAGTGCACCAACGTGCTACCCATCCCCCTTCCCCAGCTTCTCTGTCGGGGCTGGCCTTGTCTG
 TGTCTCTCTATGCCACCGCCCTTGTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACCTGCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC
 CGTTCCTCTCCAACCTCTTTGTCTTCTTGGCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCCTTTCTCTGTTTTCTCTTCTGTCTCCCTCCCTCCCACCTTTTTCTTTCTTCTCC
 CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCTTCTTCTTCTTCTGCTGT
 TTCTTCTCTGTGTTGTTTTGTGTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAGCGATTCTCCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT
 TTGCAAGCACCTTCTCCTGTGTCCTTGGGAGCCCTGAGACTTCTTCTCTCTTGCCTCCA
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGACGCGCTCCATGCCACGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCCCACCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
 CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCCTTTAAATTAACCAATATATATATATAT
 ATTTGGAGGTCAATAATTTCCAATGGGCGGGAGGCATTAAGCACCAGCCCTGGGTCCCTAGG
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTILILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIFPFSLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSLAQVNLSPFSHPKVHMDPNYCHPSTSLHLCS
 LAWSFTRLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESFSSY
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSLCSLEDGLLGSPARLASQLLGDE
 LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
 QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
 285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCCT
GGCACCCCTCTGCTCAGTGCACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCTTTAGACAGGACAACCTGTGATATTTAGTTCCTGATGTAAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGCCACATCAAGGGATTGTATTCCCTTAAAAAAAACCAATACCAAG
AAGCCTACAATGTTGGCCCTTAGCCAAAATTCTGTTGATTTCACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGAAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT
TTAAACAATGAAAAATAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA
GAAAAATAACCACCTCAAATCTCAAGCGAGTCATTCCTCTCTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGAGCATTTCTTTGGGCAGTCTAA
AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGTACACC
TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCTGATA
ACAGTTCATTACAGTTAGCATCTCTCTTCAGAACCACTTCTCCATCTGTGACCCCTTG
ATAGTGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAAACACTCTACAGCCTACCTTAAAAATCACCAATAATTCAAACCTCTTCCAA
ATACGTGAGATCCCCAAAAAGAAAATAGAAAATACAGGAATAGTATTGCGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGAAAAAGGAAAAAC
GGATTCATTTTCCCATCGCGACTTTATGACGACAGAAATGAACCAAGTTCTGCGATTAGACA
ATGACCCGGAACCTTATGATGTGAGTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCTATGGATGACATACC
TCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCACTCA
CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGGAATCAGATAAACTAAAAGATT
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTTATTCACCAAAAAATCTTAA
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCTACCCAGGAAAGTAATAGCT
TCTTTAAAGTCTTCAAAGGTTTGGGAATTTAACTTGTCTTAATATATCTTAGGCTCAA
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSNFVSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGILLCGKRKTDTSFSHRRLYDDRNEPVLRLDNAPEPYDVVSFGNSSYYNPTLNSA
MPSEENARDGIPMDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACT**TATG**TGAAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCCTTTCATTATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTACAAAGTACT
 TCATGCCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCTGTA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG
 CAATTATTTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGCTGGGGAACGTC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCTTCCGCCTTCGTCGCAGAGACCTCTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTACAATATGACTTTAA
 CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCACTTTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAAAAACTACTAACCACTGCAAGCTCTGTCAAATTTTAGTTTAAT
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG
 GGTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
 GTTGTTTTTTTTGTGTTGTTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTGAACTTTTTGTGTAAATATA
 TCAGATCTCAACATGTGTTGTTTCTTTTGTGTTTTCATTTTGTACAACCTTCTTGAATTTAGA
 AATTACATCTTTGCAGTTCTGTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAAT
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATCTTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCACAA
 CCCTATAATAAATTTTACTCTATACAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTKELRVATQEKEGSSGRCMILLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEFNFPLVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKILASG
RYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNNRKSFRLRRRDLLLGFNKRAIDKCKWIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCAGAGCAGCCCCGGGACACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGCGGGGAGCACCAGTCTGTACGCC
 AAGGAACCTGGTCTGGGGGCACCATGGTTTCGGCGGCAGCCCCAGCCTCCTCATCTTCTG
 TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG
 GGCCCATCACCCCCACCAACTTCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
 TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
 GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCCTTCAGTGAGGTCCCCGACAGAGCCCC
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCACATCTTGGCCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA
 GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGCCGTGCTCAGGGGTCTTGTG
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCACG
 GAAGCCAGGGACAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG
 TGTCTTAACAGTCTCCCGGGCTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACTCCCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA
 GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCTACAGC
 ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACCTACTTTTTTAAACA
 GCTACAGGGTAAAACTCTGCAGACCCACTCTGGAATACTGCTCTTAATTTTCTGAAGG
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
 GATCAGGTTGAATGAATGGAATCTTCCTGTCTGGCCTCCAAGCAGCCTAGAAGCTGAGGG
 GCTGTGTTTAGGGGACCTCCACCTGGGGAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG
 GTGCCACAATATTGCTCAGTCTCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
 CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGCTCCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATAAATGCACCAGCACAAATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA
 AAAGA

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPTNFLDGIVDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACL LLLALCLGSGEAGPLQSGEESTGTNIG EALGHGLGDALSEGVGAIGKEAGGA
AGSKVSEALGQGTREAVGTGRVQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDEVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSGQGLGQGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWVGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGNSGGSRGDSGSESSW
GSSGTSSSGNHGSGGGNGHKGPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GSGSDNIRYRGQSSWSGGGDVAGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCTCCGGTCTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTACCG
 TGCCTTGCTGCTGGTGGAGTTTCTCTCTTTCGTGACCACTGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA
 CTCTCTCTGCTGCGCCTGCACCGGAGCTTGGTGTGTGTCGAGGAGATGAGGGGAAGAGTGGTGTTCTCTGAAACAAGC
 TGTCTGCTACTTGTCTGCTGGGCTGGCTTTCCAGATTCCACAGTCCCTGAGGACTTGTGTTCTCTGGAAGAGG
 GTCCCTCATATGCCCTTGAGGTGGACACAGTAGCCCGCAGAGCATGGCTTGGACAATGGCCCTGTGGTGGCCACG
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACATGCTCGCTTGTGGGTGTGAGGCAGTATGT
 GACGGAGTGGGGGCTTCATGAGGAAATAACCCCAACACTACCAACAGCTGGGAGGCCAGGCTTCCAGACCA
 GCACGGGGCTCGAGGACAGCTCGCCCGAGGCTTTTCCACAACACGCCGCCCTCTTTCGCCGCGAGCCGTAGAGT
 TCGTGGCAGAAAGATTGGATCGACTGTGTCAACAATATCAAGGCTACACTGGTGGAGATCTGGTGCGCCAGG
 CAGAGTCACCTTCTCCAGAGCAGCTGGTGACACAGGAGAGGAAGGGGAGAGCCAGCCAGCTGTTGGAGATCT
 TGTGTTCCAGCTGTGCCCTCACGGGGCCAGGCAATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTCCAGAGGAGAGCCCGGCGAGCCGTTCTGAGCAGTGCAGAGAACATTGTCTGGGGC
 TTGCAACAGAGAAGGCTGTGCTTGGCTGTGAGCCAACATCAGACCACTGATCAGGAGGGAGGTGAAAGCAGCAG
 TGAGTCGACACATTCGAGGCCAGGCTCCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGGCCCTGAGC
 GTGCTCTCCTTGGCCCTGGGGCCACGGGACCCCTGACGAGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGGCAGCAGCTGCGGTGCCGCCAGTTCCCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG
 GAGTTAGCTTCCCTCCTCTCTTTCAGATCAAAATTCCTATCTAGGGCCCCGGGCACAGTACAGGCTGGAGAGAGG
 CAGGCTGAAGGCTTCTGCACATCTGCTGCTTTCCCTTGTGGAAGGAAGACTTTGAGGGGCGGCTGCTCGCTCGAGCT
 CTGCTGAGGCCAAAGAATTGGGGCTTCTGGCAGACACAAGGCCAGGAGGTGGAGCTGCTGCTATTCTGTGCTA
 CGGGAGCTGGTGGAGAGGGTCTGATGGGACGGATGAGATAGAGGCTGCCTGGCGAGCTCCACAGGCCCCAG
 TGGCCAGGGGACTTGTCTGAAGAATTAGCAACACTGTCTAATCTGTTCTTAGGCCAGGCCCAACTGCCAGAACC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGCACTGTGCTGGCCAGAGCTAGGCGTGAGAAGTGGCC
 CTGCTTGGGCATTCACCAAGACCTGAGCCCGGCCCTCAGGAGGAGGCCAAGTGCCCAATGCAGACCCCTCAC
 TGTGTTGGGTGTACCTGGCTCTACAGCTCAGACTTCCTGCTTAAGGGTGTCACTGCTTGGCATCCGACCCAGCGGA
 ATCTAGAGGAGGAGAGGATGGGCTGATTTGGGATATGGCAGAAAAGTCAGAGATGCCAGTCTCTGAGTAGAA
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAATAGGTTGTGTGGCTTGTCAACACAGATCTCAAGCTCCT
 CATTTGCTATCCAGCATCTCTAAAACCTTTGTAGTCTTGAATCTATGACAGAGGCAAAATGACTCCTGCTTAAC
 TTATGAAGAAAGTTAAAAACATGAATCTTGGAGTCTACATTTTCTTATCACCAGGAGTGGACTGGCCATCTCCTT
 ATAAATGCCCTAACACAGGCGGGTCTGGTGGCTCATGCCGTGAATCCAGCACTTTAGAGGGCTGAGGTGCGGG
 GACTGCCCTGAGGTCAGGAATTCAGACACAGGCTGGCCAACTGGCAAAACCCATCTCTACTAAAAATAAAAAA
 TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCAGCACTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC
 CTGGAGGTGGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCACCTCAGTGTGGGTAAAGAGGCGAGACTTTCTAG
 AAAAAACCTTAACAAACAGATAAGGTAGGACTCAACCACTGAACACTGACTTTCCCCCTGTACCTTCAGCCCTGT
 TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGACTTTTATAAATAAA
 CTGGTTTCTTTTAAAAAATAAAAAAAGGGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
 TTTTTTTTTTTTTTTTTTAAAAAGGGCTTTTATAAAAATTCTCCCCACAGATGGCTCCTGCAATCTGCCACAGCTC
 TGGGGCGTGTCTGTAGGGAAGGCCCTGTTTCCCTGAGCGGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG
 GCCGTGCTGGCCGCTGGCTGTGTCTAGCTGCTTCTTGGCGGCGACAGGCTGCGGGGTCTGGGGGCAACCGG
 AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCTCTCTTAAACGACACCTCGAGGTGCTCTGAGATGCTG
 GGTCCACCTTGAGTGGCAGCGGAGCAGCTGTGGCGGTGCTCTCTYTAGCGGCTCTTGGGGAACATAAGCTC
 GGGCCCTTCTTTGCAAGACCGAGGATGGGGTGGGTGTGGGGGACTCATGGGGAATGGCTGAGGAGCTAGCTG
 GAAGAGGTCGCGGTTTGTGGCTGACGCGGCTCGAGCGCTCTGCTTGGCCCTCAGTTTCCCTTTCGCTCTA
 ATGAAGAATCATGCCGTCTCGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTTGGACAGAGCTCAT
 GTTATTCTTCAACATGTCTCGCAGACTTGGCTGGGCAGCTCATGGAATGGCCATGTCCCTCTGCTGCGTGGAC
 GTCCGCGTGGGAGTGGCAGCCAGAGGCGGGGCCAGAGCTGCGCTGGGGGTGAGGGGAGGCGCCCGGAGGG
 CCTCACAGAAATTTGGGCTTCCCGCACCACAGGCGAGGGCGGGCTCCGCGCGCCGCGCACACGCTCCAGG
 GGC CGGTAGACAAGTGAAGTCCGCTTGGGCTCGCTGCGCAGAGGTAGCCCTTGATGCACTGCGGCACGCGG
 TCTGCCGAGCTGGAAGCAGCGCCGCTCCACCAGCACGAACGCCGTGCGCT

FIGURE 32

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
 SLRRTVEFVAERIGSNCKVHKIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAGLATEKACAWLSANITAL
 IRREVKAASRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCTGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGCCACAGCAGTTCCCTGCAGCTTCCCTTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACTGTGAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCTGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAAATGAGGTCTTCCATTACGGCTCCCTTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
 AACAGACACTGCCCTCTCGGTGCCACAGTGTTGTATTGTACGACAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGCTGTGGGCCATTCC
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCTCTGTGCGTGTGATCC
 AGCGAGCGGGCTGTGTTTCCCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGATGCGG
 CAATTTGACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGTTTACCATGGTGATCGCGGTGGAGTTGTGTACACAGCTGCATGTCTATG
 GCATGGTCCCCCAACTACTGACGCCAGCGGCCCGCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGAGCAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCAACCCGCTTCATCACCGAGAAAAGGGTCTTCTCATCTGTGGGCCAGCTGTATGGCA
 TCACCTTCTCCACCCCTCCTGGACCT**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGACCATCTTCTGGCCATCAAGGCTTG
 CTGGAGTGCTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGAATCTGTGTGGCAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGCTTTTC
 TTGTGCAGTCAGGGTCTGCCACAGTCAATCAGGGTAGAGGGGTATTCTGAGTCAATCTG
 AGGCTAAGGACATGTCCTTTCCATGAGGCCCTTGTTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTGGGTGTG
 CCCCCTCAATTTCCAGCACAGAAAAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC
 GGGCAGAGAATTTGTGGGGTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA
 GGCTGGCATCCAGGCTTGGCTCTGCCCTGAGACCTTGACAAACCCCTCCCCCTCTCTGGG
 CACCTTCTGCCCCACACAGTTTCCAGTGCGGAGTCTGAGACCTTTCCACCTCCCCACAA
 GTGCCCTCGGGTCTGTCTCCCGTCTGGACCTCCACAGCCATATCCCTTGCTGGAAGGCT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCACCTCCTGGAAAACTTTAGGGTATTTTTGC
 GCAAACTCCTTCAGGTTTGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCCCTACGCCAGCTGCCATTAGCTTGGCTCTTAAAGGCCAGGCCTCCTTTCTGCCCT
 CTAGCAGGAGGTTTTCCAACTGTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
 CTGGGGCTTCCGAGGCTCTCCCTCGACCTCTGTGCTCCTGGGATGGCTGTGGGAGCTGT
 ATCACTGGGTTCTGTCCCTGGCTCTGTATCAGGCATTTTATAAGACTGGGCTCAGTGG
 GGTGTGTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTACGAGGAGGCTGTGA
 GGCTGGAGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTG
 GGGCGGTGACTGCCCCAGCTGGTTTTGTAAATGATTGTACAGGAATAAACACACTACGC
 TCCGGA

FIGURE 34

MSSNKEQRSADVILFALITILILYSSNSANEVVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
 GNKTLPSRCHQCIVIVSSSSHLLGTLKGPEIERAECTIRMNDAPT TGYSADVGNKTTYRVVAH
 SSVFRVLRRPQEFVNRTPETVFIFWGPSPKMQKPGSLVRVIQRAGLVFPNMEAYAVSPGRM
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRPRLQRMPIH
 YYEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCCTCATAGTTGSGCGTCTTCTAAAGGAAAAACACTAAATGAGGAACCTCAGCGGACCGGGAGCGCAGCGTT
 GAGGGAGACCTCCCTAGCTTTTGGCGCAGAGGGCGAGGCTGAAGCCCGAGTGTGCTCCGAGGTTGTCTGAGGGCTGG
 GCGAAGCTGAACACTTTTCAACAACAGCTTCTCTGAAACCCATGACCCATGAAGTCTTGTGCACATTATAACCTGT
 CTGAGGCTGACAGCTCGAATCTAGAAGAAGTGGAGTGTGGCAGGAGCGGCATATCTTTTGTGTGACCTTGGCG
 GCGCTATGGGACCTTGGCTTGCAGCTTTTGTGATACCCATGCTGCTGCTGGGACGATGACGGCGTGGAGAGGAAT
 AGGCTGTAGGTTCACTAGCTGGCTTGCTCTCTTACGCCACAGCGGTGCTTTGCTGACTTGAACGAGGTCCTCTAG
 CTCACCGTCCAGCTTCGCTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTTGGCTGCGTGGTGGGACCTCCA
 AGGATGAATGTAACTTGGCGCTGAATGAAGAGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTCTGCTCATCACC
 CAGCGGACCTCTGCTCATCTAGCTGCCCTTAACAACCACTCTGGGACGCTACAGTGTGTGGCCCGGATGCTCGGCT
 GGGGCTTGTGGCCAGCTTGGCCAGCATCTGACACTAGCCAACTCCAGGACTTCAAGTTAGATGTGTGCAGCACTGT
 ATTGAAGTGGATGAGGGAACACAGACGATCATTGCTGCCACTGCTGAGAGGCCACCCCAAGCCGAGTCCGG
 TACAGCGTCAAAACAAGAGTGGCTGGAGGCCCTCCAGAGGTAACTACCTGATCATGCGCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCTCAACCCGATGACCCAGGAAGTGAAGAAC
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCGAGCGCC
 CAACCATCATCTGTCACCAAGGGCCAGATCTCATTTCTGGAGTGTGTGGCCAGTGGAAATCCACCCCCACGCGCT
 CACTGGCCCAAGATGGGTCACTGTGTCACCGCTACAAAGACGCGCTTCTGCTGAGCAACTCTTCCATGAG
 ACCACAGCAGGAGGAGACTCAGGCACTTACCCTGCTCATGCGCCGAATGGGTTGGGACGCCCGGACGCGCT
 ATCTCTCAATGTTCAGTGTGTTGAACCTCTGAGTGCACATGAGACTATCCGAGTGTGTCTGCTGAGCGCT
 CAGAGTGCACAGCTTACCTGTGAGGTGCTGGGAAACCCCGCGCTTCCGCTGTGTGCTGAGGAACTGTGTGTCGCC
 CTATCTTCCAGCAGCGCTTCCGCTCTCCCGAGGGCCCTGCGCTGCTCAGCATGGGGCTGAGGAGGAAGGC
 GTCTACCATGTGATTCGCCGAGAAGCAGGTTGGGAGCGCCATGCGCTAGTCAGCTGGAGACCTCAGGCCAAGC
 AATACCCCAAGGCTTGGCAGGATGCTGAGCTGGCTACTGGCACACTCTGTATACACCTCCAAACTCGGCAAC
 CTTGAGCAGACTCTGAGGGGGCAACCGGCGCTCCCGACGCCCAACGTCAGTGGGGCTGCTTCCCGAAGTGT
 CCAGGAGGAAGGGGGCAGGGGGCTCCCGCGAGGCTCCCATCATCTCAGCTCGCCCGCAGCTTCAAGACAGAC
 TCATATGAATGGTGTGGCGGCTCGGCATGAGGCGAGTGGCCGGCCCAATCTTACTATGTGTGAACAC
 CGCAAGCAGGTCAAAATCTCTCTGACGATTTGGACCATCTCTGCACTTCCAGCCACACGACGCGCTGACCTC
 ACCAGCTTGACCCCGGGAGCTTGTATGAAGTGGAGTGGCAGCTTACAAGTGTGGGGGAGAGGCCGACAGCGC
 ATGGCTCACCTTCCGAATGGACGCGCGGCCAAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC
 GACCTTGGACCGACTCCCGAGGACGAGCCAGCCAGACACCGCGCGCTCTCCCGCCAGGCTTCCCGCAGG
 CCAACCATCTCCACCGCGCTCCGAGACCTCAGTGTAGCTGACCTGGAATCCCGCTGGGATGTGGGTTCCCGCAGG
 CAGTCTCTTCTGTGGAGTACAGAAGCTAAGAGAAGTGGGAGACTGGATCTTGTGCTGCCACGAGCGCATCCCGCA
 CTCGCGCTGCTCGCTGAGATACGCGGCTAGAGAAGGCACTCTCAAGTGTGCCACGAGCGCATCCCGCA
 CTGGGCGAGCGAGCCCGCGCGCTCTCGCGCTTACGTGTGTGCGGCTACACGCGTCCGCTGTAGCAGAGG
 CCGCTGAGGCTCTTATATCACTCTCACGGATGCGGTCAATGAGACCACTCATGCTCAAGTGGATGTACATC
 CGACGAAGTAAACAACAACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTACAAATGATAGT
 GACTACAAGAAGGATATTGGTGAAGGGGACAAGTACTGGCACTCCATCAGCCACTCAGCCACAGACCTCCCTAC
 GACATTAAGATCAGTGTCTCAATGAAGAGGGGAGAGCGAGTTGAGCAACGATGATGTCTGTAGACCAAAAGCT
 CGGAAGTCTTCTGGCGAGCTGCTGACTGCCACCCCAACTCTGGCCCAACACAGCGCCGCTCTTCTGAAACC
 ATAGACGCGCGCGTGGGCACTGGGCGCATGTTGGCTCGCTCCAGGCACTTGCCTATCTGATTCTCGGGTGTGCT
 CTGGGCTCATGCTTCTCATCTGCTCACTTCTATCCCTTCTGCTTGTGGGGGCGCTGGTCTAAGCAAAAACAT
 ACAACAGCACTGGGTTTTCTCGAAGTGGCTTCCACCTCTTCCCGCTATACATATGTTGGCTTGGGAGGACT
 CCAGGCCACCGGCGAGTGGACAGCCCTACCTCAGTGGCATCAGTGGAGCGGCTGTGCTAATGGGATCCAGT
 AATAGAGGCTCGCCCTCGCTCAGTGGGCTACCCGGGCAAGGCCCCAGCAGCTCCCGGCGAGCTCTTCAAG
 CAGGAGTGCACCCAGCAGCGCTGCTGAGGACAGCCCATCTTGGCATGGATTTATGACCTTGAACGACCTCTCAG
 ACGAGGGTCTCCAGTCTAGCGGAGCAGGCTCTTCTTATACACTGCCAGCTTCCGACAGCTCACTCAGCAGT
 CTGCGCCCATCTCAGCTGCTGCCACGCGAGGACGCTCTGCTGTGGGCACTCAGGGGTGAGGAGAGCG
 CCGACAGTCTCTCTTGAAGACACTGTGGACCTTCCATTTGACTCAGGCGCCCATGCTGCTTGGCGCTTGTG
 CCTAGTGAAGAGGTGCACAGCTCTGACTCTCTGCCAAGTGAAGTGGAGGAGCTGGTGTCCCGACGACCCGTAGG
 GCGCTAGTAGCAGGAACTCGAATGCACTCTCCCGGCGCACTGGTGTGCTTGTGAAACACCACT
 CTCACATTTAGGCGAGAAGTATATCCGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAGAAAA
 AGACACAGAGAATAATTTGGTATTTATTTTCTATTTATAGCCATATTTATATTTATGCACTTTAATAAATGT
 TATGTTTTATATTTCTGGAGAGACATAAGAGTCTTACCGTTGAGGTTGAGAGGGAAAAATGAAGAGCTGCCA
 CTTAACAGGAGTCACTCCAGGAAGACCGCAGCGCTGGCGGCGGACAGACTCTAACCTGGGCGCTCTCGAGT
 CGAGGCGAGGCTCGAGGAGGCCACAGATAAGCTGGCAAGGAGAAAGATCCAGGACATGTTTCATCAGAGCA
 TGAAGGAACAGCAAGGGGACGCTATCAGAGCTGGAGACACCAACAGATGCTGATTCGCTGCTACGGGAA
 ACATTTTTCTAAGATGCCATGAGAACAGCCAAAGATGTGACAGACATGAGCATTTAAAAACCTTCCGAAT
 CAATATCTCGTGGCAACTATCTCTGTAAGAACAAACATGTAACCTTCAATTAAGTTTAAAGTCTTCCCTGTA

FIGURE 36

MLRGTMTAWRGRPEVTLACLALLATAGCFADLNEVPQVTVQASTVQKPGGTIVILGCVVEPP
 RMNVTWRNLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSTGNLQ
 IVNASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIYPPAQTIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGGQGA
 AVILYNVQVFPEPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQCMANEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGQGAPAEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASQSSSQPDHGRSLPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESESPASRPYVVSIGYSGRVYERPVGAPYITFTDAVNETTIMLKWMIIPASNNNT
 PIHGFIYYRPTDSNDSDYKKDMVEGDKYWSHLSHLQPETSYDIKMQCFNEGGESEFSNMV
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVTGAMVARSSDLPYLIVGVVLGSLVL
 IIVTFIPFCLWRAWSKQKHTTDLGFPRSAIPSPCYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMRGCPSSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK
 SSPDEGSFLYTLRDDSTHQLLQPHHDCCQRQEQAAGVQSGVRRAPDSPVLEAVWDPPFHS
 PPCCGLGLPVVEVDSPDCQVSGGDWCQHPVGGAYVQEPGMQLSPGLVRVVSFETPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCCACGGGCCGCGAGGGTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGGCTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGTCCCCC
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTACGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTACCCGCATGTGTGCTCCTACTCTGAACCTCGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACCCATGGGCAGAGAGTTCACCAAGTTACAGACAC
 CACATGTACACCAACGTGACGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCTTATGCATCGGACACCTTGATAAGAAGGGTCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAAATATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAAACCAATCGGGTCCCCTGGAGGTCCTCAAATGCCT
 CCCCATACTTGTTCAGGCCTTGTGGCTGTGCCACCATCCCAACCTTCACCCAGTGGCTC
 TGCT**GAC**ACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGA AAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPTKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQC�LLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFPYQLSTSCH
SHLVFPQNGHQATHLEVTQFTNRVFWRSSNASPYLVPGLVAAATIPFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTTGGTGGCTGTGGTCCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
 TTTACAACCAGAAATGTATCCAGAAAGGACTGCAACTGCCTGCACGTGTTGGAGCCCATGCCA
 GTGCTTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGTCTATCTTGTCTATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCAACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCTTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTCTCTCCTT
 CTCCTTAACCTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
 GATCTCTGTTGTCTTCTTGGGTCTTGGGGTTGAAGGAGGGGGAAGGCAGGCCAGAAGGA
 ATGGAGACATTTCGAGGCGGCCTCAGGAGTGGATGCCATCTGTCTCTCTGGCTCCACTCTTG
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCTTGGAAAGATAAAGCTGGGTCTTCA
 GGAACCTAGTGTCTGGGAGGAAAGCATGGCCAGCATTCAGCATGTGTTCTCTTCTGCAGTG
 GTTCTTATCACCACCTCCCTCCAGCCCCGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACCTGGGTCTTCAGGGTGCACTGGA
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGGCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACCTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGT
 CACAGTCACTGAGCCAGACGGTCCGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCGTACTTGGGTTGCCTTGTCCCTGAACTTCGTTGTACCAAGTGCATGGA
 GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG
 TTTTATTTCTCTCA

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHDEV EAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
 ACCAGGAAGGGTTGAGGGAAACAAATCTGCAAGCCCCGCGACCCAACTGAGGGGCCCGTGTGGGGTCTCTCC
 TCCCTTTGCATTTCCACCCCTCCGGGCTTTCGCTCTTCTCGGGGACCCCTCGCCGGGAATGGCCGGTGTATG
 CGGAGCAAGGATTCGTCCTGCTGCCTGCTCTACTGGCCGCGGTGCTGATGGTGAGAGCTCACAGATCGGCAT
 TCGCGGGGCCAAATCAACTCCATCAGTCTCTCTGGGCGGGGAGACGCCTGTCGAGCCGCCAATCGATCTGCG
 GGCATGTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGGCAAAACCTGGGGCAGGCTACCTCTTTAGCAGT
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCCTGCATGGTGTGCGAGA
 AAAAAAGAGCGCTGCCACCAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATATGGCATCTGTATCCGAGTT
 ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAGCGTCATTAC
 TCAAPCCATGACTTGGGATGGCAGAAATCTAGGAAGACCACACACTAAGATGTACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
 CCAGTGTCCATCAGGGGGAAGTCTGTACCAAAACAACGCAAGAAGGGTTCTCATGGCTGGAAATTTTCCAGCGT
 TGCAGCTGTGCGAAGGGCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG
 TGTGAGAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
 CATGGTGGAAAATAAGGTTGAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA
 AAAGGGAGAAAGAAACATGAATGAATAGATAGAAATGGGTGACAAATGCAGTGCAGCCAGTGTTTCCATTATG
 CAACTTGTCTATGTAATAATGTACACATTTTGGAAAATGCTATTATTAAGAGAACCAAGCACAGTGGAAAT
 ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGARTAACTTGTTA
 TACAATAGGTTCTAAAAATAAAATGCTAAACAAGAAATGAAACATGGAGCATTGTTAATTTACAACAGAAAA
 TACCTTTTGATTTGTAAACACTACTTCTGCTGTTCAATCAGAGTCTTGGTAGATAGAAAAAATCAGTCAATAT
 TTTCCAAATACTTTGCAAAATAATGGCCAGTTGTTAGGAAGGCCCTTTAGGAAGACAATAAATAACAACAAACAG
 CCACAAATACTTTTTCAAAATTTTAGTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC
 TTCAGATTCTACGAATGACAGTATCTCTCTTATCTCTATCTGATTTCTGCTCTGAATGCATTATATTTTCCA
 AACATACCCATAAATTTGAGTACTGATAAATACITACACAGAGCAGAAATTTTCAGAGTGGCAAAAAATTTAAA
 GATGTCCTAATATATGTGGAAACAGCTAACAGAGAGATCATATTCTCTAAGATTTGGCCATAACCTTATTTT
 GATAGATTAGATTCTGGGATAACATGCTATTATACATACACTCTGTGGTAAAGACTTGAAGTGGATCTGTACTG
 CACTGGAGTAGCAAGAAAATTTGGGAAAACTTTTCTCTTGTGTCAGTTTGGCAACACATAGATCATATGTCGT
 AGGCACAAGTTGGCTGTCACTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTCATGGGATTTTGCAT
 CATAATATTTACTATGCAGATGAATCAGTGTGAGGTCCTGTGTCGGTACTATCTCCTAAATTTATTTATTTATAG
 TGCTGAGATCCTCAATATATCTCAATTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGATAGTGAGG
 TTTCAITGGCCCTATAAGCTTCTGACTAGGCAATGGCATCATCCAATTTCTTCCCAACCTCTGCAGCATCTG
 CTTTATTGCCAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAGTAGGATAACTTGTAAA
 ACCGTCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTGAAACCACCTTTACTACTTTTAAAACT
 AACTCAGTTCTAAATCTTTGTCTGGAGCACAAACAAATAAAGGTTATCTTATAGTCTGAGCTTTAACTTTTG
 TAGACCACAATTCACTTTTTAGTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAAATTTAAGTTCTCCAGTAG
 AGATTGAGTTTGAAGCTGTATATCTATTTAAAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA
 CATTTTTCTGCACAGGCTGCAAAAAACAAAAATTTATAAATAGTCCATCCCAAGAACCAAGTTTGTATAACAGGT
 TGCTATAAGCTTGTGAATGAAAATGGAACCTTTCAATCAACATTTTCTATATAACAATTTATATATTTCAAT
 TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTTATTTTGAAGTAATTTTATTTACAGGAATG
 TTAATGAGATGATTTTCTTATAGATATTTCTTACAGAAAGCTTTGTAGCAGATATATTTTGCAGCTATTGAC
 TTTGTAAATTTAGAAAAATGTATAATAAGATAAAATCTATTAAATTTTCTCCTCTAAAAAAGTAAAAA
 AAAAAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSTIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAA
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGCCAACATCACGTTTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
 TTTAAAGTCATCCGTCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACA
 TCACCAGCTCCCAGATTTTGGACAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACCTACTACTTCTTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT
 CCTGGTTTGGAGTCCTTCTCTCCAGGCAAACTTCGAGAATCAACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGCTG
 TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGCGGATACCCCCAGCTTCTAAG
 ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATTCCCATCAGCTTGTATTGCAAGTCTTTAAGTGAGCCTTTGAATACA
 TCTTTATCAATGACCAGTGCAGTACAGAATCCACATATACAACCTCCGTCATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCGCTAGTCCAGTAGCAATGTCTCTCTCTTATGACC
 AGAGTTCGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
 GGAACCATCATGAATGGACATGGTGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTTGTGCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
 TGTGGAAAACACCAGTTGGTCAATGGCTCATTGCTTAAAGCAGCCCTTTTGCTTTTTTGT
 TTTTGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTCGAGCATACAGTATGCAT
 TTTAAAGATGCTTGGGCCAGGCGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTC
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGCGCGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSDWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP
PGLSEFSPQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

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FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT
 TTGGAACCTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCGCGCTGGAGGTCACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGGGCGCACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCGGG
 GTCCCGCACGACCGCGCGGACCGCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
 CGGGCCCCCTTTTCTGCGCGACCGCTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGCTCTCCACCTGACGGTCGCGGAACCCACGC
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTCAATGTATCGTCCCCGAGAGCCGAGCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTTTCATCCTGCTACTGCTC
 TGTCTCCTGGCGCCCGCAGGCGCGCGGAGGCTACGAATACTCGGACCAAGAAGTCGGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAAGGGACCATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCACTGATGCCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCTG
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTACGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTCGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGGCTGTGTTGCCACTCTCAGCACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCATCTGATTTTTAAAAA
 AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWD RQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGDFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPNGSSHS GAPGDPPTLARGHNVIN VIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKGDVNLA EFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLKGFRENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGCGGCGTGGCGCAGCGCGCAC**ATG**CGCGTGTGTCTCAGAGGACGACTTT
CAGCACAGTCTCAAACCTCCACATCGGAAACCCACAGCAGCAGTCTCCGAGCTGACCAAGGAGG
ACTGCTTTGAGAAGCTGCTGGACGCCCGCCCTCTGGCTGCAGAGGCCGAGACCGCTTCT
GTGGCACATACATCATCTTCTTACGCTGGGCATTGGCAGTCTACTGCCATGGAACCTTTT
ATCATCTGCCAAGGAGTATGTGATGTCTCAAACCTCCGACATCTCCAGCCAGCCAGCCGGGTA
GGACCTTGAGGCTGACAGACTCTGAACACTACTTTGAGAGCTACTCTGGCTTGGCTCCACCG
TGCCCTCCATGCTGTGCTTGGTGCCAACTTCTCTGCTTGTCAACAGGATGCGACTCCACAT
CGTGTCTCTGGCCCTACATGACGGCTATCTGGCCACTCTCATGGTAGTAATGCTGACTGGTGA
GGTGAGACACTTCTCTGGACCGGTGTTTTTTTGGCGTACCATTGCTGTGCATGGTGATCC
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATACGCGGCTTCTTCTCCATATG
AGGAACCTCCCAAGCAGCTGATATCAGGAGGAGGCCATGGGCGGGACGGTGACGCCCTGTGCCCT
ATTGGTGGAATTTGGCTGCATCCAGTGATGTAGGAACAGCGCCCTGGCCTTCTCTCCGAGCG
CCACCATCTTCTCTGTGCTCTGTCATGGGAATCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCCTGTTCTTGGCGCCCATGTGTTTTTCTGGTGGAAGAGAGCTTCCCCA
GGACTCCCTCAGTGGCCCTTCGGTGCCCTCCAGATTCATTGATTCACACACCCCTCTCC
GCCCATCTCTGAAGAAGCAGCCAGCCTGGGCTTCTGTGTCAACACTAGCTTCTCTCATACC
AGCCTCATCTACCCCGCGCTCTGCAACCAACTCAGATCCCTCAACAGGGCTCGGCTCATCT
GTGGACCAACCAAGTTTTTCATCCCCCTCACTACCTTCTCTCTGTACAACCTTGTGTGACCTAT
GTGGCGCGGAGCTTCAACGCCCTGGATCCAGGTGCCAGGCGCCACAGCAAGGCCCTCCAGGG
TTCTGCTCTCCGAGACTGCTCATCCCTCTCTGCTGTCTGTAACACTACAGCCCGCGCT
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCTCAGCTCCTGTGCTGG
GGCTCAGCAACGGCTACTCCAGCACCTGGCCCTCCTCTACGGGCGCTAAGATTGTGCCGAG
GAGCTGGCTTGAGGCCACGGGATGGTGATGTCCTTTTATGTGTGCTGGGCTTAACACTGG
CTCAGCCTGCTCTACCCTCCTGGTGACCTCAT**TAGA**AGGGAGGACACAAGGAGATTTGGTG
CTCTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAAGGAGGCTGGGGCCATGGAGGAAGGCC
TAAAGTTTCACTTTGGGGACAGAGACAGACATCTCGGCCATCTCCCTCCAAGATGCCA
GTGAGCAGCTCCATGCCCATTCCTGTGCAAGGACAGATATTCAGTACATATTAAACAGCAACT
CCTGAGACAGTGTGAAGAAGAAATGCAACAATCAGGGGTACTCCCTCATACGTTAGTGTTA
ACATTCCACCTTCTTCTAGCCCTCAAAGATGCTGCCAGTGTCGCCCTAGAGTTATTACA
AAGCAGTGCACAAACCCAGCATGGGCTCTTGAACACTCCAGCTGCGCTCATTCACAGT
GACACGAGATGCAAGCAAATGCTCAGCTCTCTTACCTGGAAGGGGTCTCCTTGAATGGA
AGTCCCTTGGCATGGTGACGTCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
GCGGGTGAAACACTGCCCATTAACAGACTGAAAAACCAAGAGATGGGCTCTCCATGAAT
GCTTATTCCAGAGGAGACAGAGGCTCCTCTGTGCAAGGGATCAAGCATGTCTGGCTGGG
TTTTCAA AAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGGTC
TTTACGTTTCTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAAA

FIGURE 48

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPGLQRPEDRFCGTYYIFFSLGI
GSLLPWNFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRSALAFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITSLIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 50

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDDPYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLS DAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLG YALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMS EDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPV VAMTQGPHDVHVQIETSPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFR RPFWREEHIEGG
HSNTDRPSRMIFYPPPPREGALLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHG VASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCCTTCTGCCTGCAT
 GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCAAGCAGGCGAGGAAGAGGACAGGACTCTGGTGGCAGGAA
 GAACCTCAGAGCGGGGAAGCCCCATTCTACTAGAAGCACTGAGAGATGGCGGCCCTCTCGCAGGCTCTGAATTTCTCT
 GCTGCTGTTACAAAGATGCTTTTATCTTTAACTTTTGTTCCTCCCACTTCGACCCCGGGCTGTGATCTGCAT
 CCTGCACATTGGAGCTGCCATCTCTTGTGGCTGATCACCAGACCTCAACCCGCTTACCTCTCTTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCAGCGAAGGGGGTTTCCAGAAGAACAATGACCTAACAGTGTCTG
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTGCTGTGCTGACATCTTTGCTCAGAAATAGGCCAGAGT
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGTGTCTGATAGACAGAGTACTCTGGGTTC
 CTGTCTCTGCAATAAAGGTTATAAATCATCACCAGACCACTTGTGGCCTACTTTGCTCAGAAATAGGCCAGAGT
 GATCATCTCCGAATTGGCTTGTACAGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTTGGGACCAGAAGC
 CATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATTGGTGTGAT
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCTTATGACCCCTTTGTATGATGACCTGAA
 GCAAAGAGGGGAGAGAGTGGAAATTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCCAAGAGCACTT CAG
 AAAACCTGTGCCCTCTAGCCCAGAAGCCTGAGCGTCTATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTCCTTTCTCAAAATGTGTGGAGCATGCTTATGAGCC
 CACTCTGATGATGTGGCCATATCTTACCTCCCTCTGGCTCATATGTTTGAGAGGATGTACAGGCTGTTGTGTGA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTGTTTCCCGCGGTGCCCTGCACTCCTTAAACAGGATCTACGATAGGTTACAAATAGGGCCAAAGACACCCCT
 GAAGAAGTCTTGTGTTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTGTGCAAAAGATCCAGGACAGCTGGCGGGAAGGGTCTGCTGTAATGTCTACGAGC
 TGCCCCCATGTCCACTTTCAGTCAATGACATCTTCTCGGGCAGCAATGGATCTCAGGTGATCAAGCTTATGCTCA
 AACAGAAATGCACAGGTGGCTGTACATTTACATTACCTGGGACTGGACATCAGTCACTTTGGGGTCTGCTTGGC
 TTGCAATTACGTGAAGCTGGAGATGTGGCTGACATGAACACTACTTTACAGTGAATATGAAGGAGAGCTTCTGCAT
 CAGGGGTACAAACGCTGTTCAAAGGATACCTGAAGGACCTGAGAAGACACAGGAAGCCCTGGACAGTGTATGGCTG
 GGTTTACACAGGAGCAATGGTCGCTGGCTGCCGAATGGAACTCTGAAGATCATCAGGCTGTAAGGGAACATTTT
 CAAAGCTGGCCCCAAGGAGATACATTGCACCAGAGAAGATAGAAAATATCTACACAGAGGAGTCAACCAAGTGTACA
 AATTTTGTCTACACGGGAGAGCTTACCGTCTCTTATGATAGGAGTGTGGTTCCTGACACAGATGTACTTCCCTC
 ATTTGCAGCCAAAGCTTGGGGTGAAGGGCTCCTTGAGGAACTGTGCCAAAACCAAGTTGAAGGGAAGCCATTTT
 AGAAGACTTSCAGAAAATTTGGGAAGAAAGTGGCCCTTAAAACTTTTGAAACAGGTCAAAGCCATTTTCTTCACTCC
 AGAGCCATTTCTCATTTGAAAAATGGGCTCTTGACACCAACATTTGAAGCAAAAGCGAGGAGAGCTTCTCAAATACTT
 TCGGAGCCAAATTTGACAGCCTGTATGAGCACATCCAGGATTAGCATAAAGTACTTAAGTACCTGCGCGGCCACTG
 TGCAGTCTCTGTGAGAAAATGGATTAAAAACTATTCTTACATTGTTTTCGCTTCCCTCATTATTTTTTTAAACC
 TGTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAATGTGTAACCTTAGTTCCTCAAATTAATCA
 ATCTCTGTTTCCCATCTTCGATGTTGCTTAATATTAAGGCTTCAGGCTACTTTTATCAACATGCTCTCTTCAA
 GATCCCAGTTTATGTTCTGTGCTTCTCATGATTTCCAACTCTAATACTATTAGTAACCAACAGTCTCAAGGCT
 CAAAGGACCCCTCTGTGCTCTCTCTTTGTTTGTATGAACATAACTTGGCCACAGTCTCATGTGCTTATTTTACA
 TCTTCTACTGTTCAAACATAAGAGATTTTAAATCTGAAAAACTGCTTACAAATCATGTTTCTAGCCACTCCAC
 AAACCATAAAAATTTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT
 CTGCGCTAAATTAATTTGTGACTGAAGGGAAAGTTTGATCATACCAAACTTCTTAACTCTCTAGTTAGATA
 CTCGACTTGGGAGTATTAATAATTTGGGCTCATGACATCTGTCCAAAAGGAATTCGTTCTTAAAGCATTTATTA
 CAGTAGGAACGTGGGAGTAAATCTGTTCCCTACAGTTTGTCTGTAGCTGGAAGCTGTGGGGGAAGGAGTTGACA
 GGTGGGCCCACTGAACTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACTCTGAACTGGGAACAAAGATCT
 ACAGGCAAGCAAGATGCCACAACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCTTGGATT
 AGAGTTCCTGCTCACTTACCACAGATAACACATGTTTCTTACTTGTAAATGTAAAGTCTTTAAAAATAAC
 TATTACAGATAAAAAA

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 52

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAIFLWLITRPQVLPFLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRLAVSDNGPCLGYRKPNQPYRWLSYQVSDRAEYLGSCILLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPFAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAAFKLCVEHAYEPTDDVAISYLP LAHMFERIVQ
AVVYSCGARVGGFQGGDIRLLADDMKTLKPTLFFAVPRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLI FAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTS GHVGVPLACNYVKLEVDADMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNI FKL AQGEYIAPEKIENIYNR
SQPV LQIFVHGESLRSSSLGVVVPTDVLPSFAAKLGVKGSFEELCQNQV VREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSSIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGGCCCTAGCGGGGCCCGAGCGGGG
 CCCGGGGCCCTAAGCCATTCTCTGAAGTCAATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGTATGGACGACTGGAAGCCCGAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAACCGG
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGGCCGTGCTTTTCTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCTTGGACA
 CTCGGCGAGCCATCAGTGAAGCCCAATGAAGACCCAGGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTTGAGCCCCACGGCGCAGAGGCACTGGTCCCCGGCGGGTCTTGGACGCTAGA
 GGTGTATTCAAGTCGACGAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGCGCATCCATGTCAATTGTCTCCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAAACGTGTGTTTGACACGTAACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCGGCGAGTGCTCATCTGCATGTCAAGGATGAGGGCTCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAGGAGGTCTGTCTTCGGGGAGAAACATTC
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCCGCGCGGC
 TTCTGCAGCAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCGAGACAACAAGGTCTCAATGTGCGCTGTGGCTGTCAATTGCAG
 GGAACCGACCCAAATTACTGTACAGGATGCTGCGCTCTCTGCTTTACGCCAGGGGGTGCT
 CCTCAGATGATAACAGTTCATTGACGGCTACTATGAGCAACCATAGGATGTGGTGCACT
 GTTTGGTCTGAGGGGATCCAGCATACTCCCATCAGCATCAAGATGCCCGCGTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTCCGGAGGCCAAGTTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTCAGTTTCTGAGCCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCTACTGTACCCTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGCCCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCTTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGAGC
 TTTCCGATCCTACCATTGCGCATCGTCGGCTCAACATGAATGGCTACTTTTACGAGGCC
 TACTTCAAGAAGCACAGTTCAACACGGTTCAGGTGTCCAGCTCAGGAATGTGACAGTCT
 GAAGAAGAAGCTTATGAAGTGAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTCTTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTTCCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTTATCGAATGGAGAAAGATGATGACTTACCACCTGGACCCAGCTTGCCAAAGTGCCTCCA
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA
 ACCACTTCTTGGTGGTGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC
 ACCCCAATTTCTCGAGCCACCCCCAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
ATGACAGCTCCTCCAGGACCTCGGGGCTGGGTACTGTGTACCCAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGATTGTTGTAGATGCTGGTAGGGCTGGGGCTACCTTGTGTTTTAACA
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCGTTCTCTGAGTT
 AAAAGTCTATTATTACTTCTTCTTGGTGGAGAAGGCCAGGAGACTCTGGGAATCATTACG
 ATCCTTAGCAGCTCATCCTGCCCCTTGAATACCTCACTTCCAGGCTGGCTCAGAATCTA
 ACCATTATTATTACTGTCTGAGGGCTTGAAACACGGCCGAACCTGAGGGCTCGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCTTA
 CAGATTGGACAGGCTCCTCTCAGCCTTCTCTTGTCAAGATTCCAAGCTGGTATAGTT
 GGTCAATGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFNLNVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDWTAFVGRKGGPVFGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRRRRRFCSKVEGYGSVCCKDPTPIEFSPDPLPDKNVLPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFIDGYEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKEAYEVEVHRLLSAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVDRGNHRGLWRLFRKKNH
FLVVGVPASPSVSKPPSVPTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC
 CTGTTTAAAGCAACTAAGCACCATTAAAGCCCACTGGAAATTTGTTGCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAAATGGGATGATTTTCATCTCCATTAGCCTGCTGCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTTCCCTTGCTGTTAATTTCTCAGAGGAACCACTGAAGCTGGTCACTGTTTTGG
 GTGCTGGCCCTTCTCTGFGAAGCTGCTCGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTCTTGAGGGAAAACACCACCAAGCAAGTGAACACATAATGTGATTGTCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCATATATTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACAGATTGGTAACTCCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAATCACCACCACGCTGGGTCTGGTTGTCCA
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCAAGACCACTGTCAGTTAATG
 TGTGTTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCTTCTTGATGCATGCT
 GGCCTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
 GGTGACATCTTAGGACTGAGTAAGAGCAGTAAAGAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTCTCTGCCCGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
 ATAGGGCAGACGCAAGGCCGATGCCACGGGAGGGAGAGGCTCAGCCGCCCTGGAAGTGGCAGCCCT
 GGTTCCTGGGTTGCCCTCATCCCTCTCATCTGTGCTAGGACACCAAGCATTAATGTTCTCAAGGTCCAGC
 CTTGGTCCAGGGCGGTTTGGCATCCAGTGCAGTGAGAACAGCCGGACGTGACAGCTACTCATCTCTCAGTC
 TCTTGTCTCACCTTGGCATCTCTACATGTATTCTAGAGTCCAGAGGGGAGGTGAGGTTAAAGCCCTG
 AGTAATGGAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAATATTTCTCTTAACCCCTATTCTCAGGGAAGATG
 GAATTTAGTTTTAAGGAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCCATGATTTTT
 AACATGGTTCCCACTATGTAAGACTGGTGCCTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATA
 GCACCCACTCACTTAGATGATCAAGGTGATTCTAGTTAATCTGGGATTAGGTCAGGAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATACTCAAAAGAGATTCATTGAAAAGGGATGTCATAGAGGAT
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCTTGTCAGTTCTCCTTTGCAGAA
 ACCTGTCTCCACATTCCTAGAGAGGAGCCAACTTCTAGTAGTTTCAAGTTCTGCTTCTCCTCAAGAA
 CAGTCAGATCACAAGTGCTTTTGGAAATTAAGGGATATTAATTTTAAGTGATTTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAAATGTATGGTGTGCCCTTTTTTTTGTGTTTT
 TTTTTTTTTAATTTATTTCTCTTAGCAGATCAGCAATCCCTTAGGGACCTAAATACTAGGTACGCTTT
 GGGACACTGTGCTTCTCACATAACCACCTGTAGCAAGATGGATCAATAAGTGAAGGTGTTTGGCTA
 TTGATTTAAAGCTTATGGAATCATGTCTCTTGTCTCTTCGCTCTTTTCTTGTCTTTCTTCTAACTTT
 TCCCCTTAGGCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAAT
 CTTATCAGGACAACCACTTCTCGAAGCTGTAATAATGAAGATAAATAATCTTTATTTCTTTATCCCTTT
 CAAAGAAATFACCTTTGTGTCAAAATGCCGCTTTGTTGAGCCCTTAAATACCACTCCTCATGTGTGA
 ATTGACACAATCACTAATCTGTAATTTAAACAATGAGATAGCAAAAGTGTTTAAACAGACTAGGATA
 ATTTTTTTTTCATATTTGCCAAATTTTGTAAACCTGTCTTGCAAAATAGTGATAATATTGTAT
 TATTAATTTATTTTACTTTCTATACCATTTCAAAACACATTACACTAAGGGGGAACCAAGACTAGTT
 TCTTCAGGCGAGTGGAGCTAGTAGTTTGTAAAAACGTTTCTATGACGCATAAGCTAGCATGCCATG
 ATTTATTTCTCTCATGAATTTGCTCACTGGATCAGCAGCTGTGGAATAAGCCTGTGAGCCCTCTGCT
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATTCATACATA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTCTGATTGGATGTTAAGAGCT
 GACTGGTGTGAGACTTGAAGTTTCATCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCGGA
 AACTGACTTTGTCAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQ
IGNSHVHSTDDPEARSSNSKITTTGLLVVHAAADGVALGAAASTSQTSTVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGGCGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
 GAAACGGGCGTGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGAGGGCGGCTGCAGAGAGAGGGCCCGTGGAGCTGAAGA
 AGAACGAGTTCACGGGAGAGCTGGAGAAGCAGCGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGCGGTTTTGGTGAA
 TAACATCACCACAGGTGAGAGGCTCATCCAGTGCTGCAAGACCAAGTTAAAGACCTTCGAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTCAACAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA
 GTCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGACGGAG
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTGAGTGAGCCAGGAAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGTTGTGATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAAACAGGGCCGAAGAGATGACTA
 TAAAAATGTTATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTTEVPQKGKGNVLGNSKSQTPAPSSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGAGAGAAAGCCTCAGTGTGCTCTTCTCGGCTGGGTCTGCTTCTCTTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCTCGCTCACCCTGTTGGAGCTCACCACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
TGCCATGGGGAGCCCAAGGGAACCTGGGGCTGCTGGATGGCTTCCGATTTTTCGGGGTTGTTGGTGGTGA
TAGATGCTCTGCGATTGACTTCGCCAGACCCAGCATTACACAGTGGCTAGAGAGCCTCTGCTCTCCCTACGCT
TCTTGGGCAAACTAAGTCTCCTTCAGAGGATCCTGGAGATTACGCCCCACCATCGCCGCTCACCAGTCTCAGG
TTGACCTCTTACCACCACTTGCAGCGCTCAAGGCCCTCACCCTGGCTCAGTGCCTACCTTATTGATGCTG
GTAGTAACCTCCGCGACCGCCATAGTGGAAACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCCGTAG
TCTTCACTGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGTCTTCTCCAAAGCTTCTCTTCCCTCCTTCA
ATGTCCAGAGCATAGACACAGTGGACAATGGCATCCTGGAAACACCTTACACCCACCTAGACAGCTGGTGAATGGA
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCATGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGCCA
AGAACTTAGCCAGATGGACAGGTGATCCAGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAAGTGGAGTCTACGTGCTCTCTTTC
TGTATAGCCCCACAGCAGTCTTCCCGACGCCACACAGAGGACCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCTGCCCATTCCTTATTTGGGAATTCGGGGAAGTGAATGGTGAAGTATTCTCAG
GGGTGAGGACTCCGAGCCCCACTCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCGATTTCTTATACCTACTCAGTCTGCTACTCAGGACCTTCAAGTGAAGAGCTTCACTCAGCTGCAGAACCTCT
TCTCCAGGCTCTGCTGACTACAGTGGCTTCTCCAGAGCCCCAAGGGGCTGAGGCGACACTGCCGACCTGTGA
TTGCTGAGCTGCAGCAGTCTTCTGGCGGGAGCTCGGGCCATGTGCATCGAGCTTGGGGCTGTTTCTCTCTGGTCC
GCATGGCGGGGGTACTGCTCTTCTGGCTGCTTCTGCTTTATCTGCTGCTCAGTCTCAGTGGGCAATATCC
CAGGCTTCCATTCTGACCTTACTCCTGACACCTGTGGGCTGGGGCTGGTGGGCGCATAGCTGATCTCCGAC
TCTCGGAACATTGACCTGAAGCTAGATCTAGTCTCTAGGGGCTGGGCTGAGCTGAGCTACTTCCCTTCT
TTCTAGTGAAGGCTGGGCTGGGCTGGGGGTCAGAGGCCCTTGGCAACCTGTTTCCCATCCCTGGGCGCTGCT
TGTTACTGCTGCTGTTTCTGCTTGGCTGTGTTCTTCTCTGATAGTTTGTGAGCTGAGGCGAGGCCACCCCT
TCTTTTGGGCTCATTCACTGCTCTGCTGCTTCTCCAGCTTCAAGTGGAGGGGCGAGCTGCTTCCACTAAGCTAC
TCAAAATGCCCGCTTGGCATCTCAGCCACACAAACCCCGACAGCATGGTGGCATATGCTGCTGAGGCTGTG
GAATTGGTGTCTTTATGTCAAGGCTAGCTGGGCTTTTCTGTTGGCCTGAAGAGACACTGTGTTGGCAT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTGCAGGCAAGAATTTATGTATGAGCTGTGTGTGG
CGCGCTGTGTGGCCTGTAGTGTGGCTGTGGCTTGTGGCTTCCCGCTATGTAATCTCAAGAGCCCCAGGCCAC
CCATGCTCTTTGTGGCTGGGACTGCCCTAATGGCATGGGTACTGCTGCTACTGGGCATGGCGTGGGGG
CAGATGAGGCTCCCCCGCTTCCGGGTCTGGTCTTGGGGCATCATGGTGTGCTGCTCGGGCTGTAGCAGGGC
TGGCTGCTTCAAGGCTCGGCTGCTGCTTCTGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCAA
GGACAGGACTGCTCCTCCTCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGTGTCTCCTCAA
TCTACCGACACATGAGGAGGAGTTCGGGGGCGGTAGAGAGGACCAATCTCAGGCTCCCTEACTGTGGCTG
CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTCAAGCCCTCACCCTGTGGCTTCCCATCTCTGCTGT
TGCATCGGAGGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCCCTCTCCTACATCTGCTGTG
CTGGGATACCGCTCACCACCCCTGGTCTTTTACTGTGCCATGGCAGGAGCTCTCGGCTTGGGCGCTCATGGCCA
CAGAGGCTTACTTCCAGGCCACACAGCCTCTTTCAGGCATCCATTGGCATGCAAGCTTCTGGGATTC
CAGAGGCTCATGGCTCTGCTACTTGGCTGCTGCTTTTGTAGTGGGAGCCAAACCTTGGCTCCCACTCTCTCT
TTGAGCTAGGTTTGGCCTGCTGCTTCTGCTTCTGCTTCTGCTGTGTGAGAGTCAAGGCTGCGGGAAGAGACAGCAGC
CCCCAGGAGTGAAGCTGATGCCAGGTGACGCCGAGGAGGAGGAGGAGCTGATGGAGATCGGGCTCCGGCT
ATCGCCTCAGCATTCTATGAGCAGCTGCTGAGCTGGGCTCAAGTACCTCTTATCCTTGGTATTCAGATTCT
TGCTGTGCTTGGCAGCTCCATCTTCTGAGGAGTCTGAGGAGTCTGAGGAGTGTGCTGATTCGCTGATTCATAT
TTGAGCTGTGGGCTTCAATTGTGAGCAGGCTGGGACTTCTCTGGGATAGCTTTGGTGTGAGAGTGGATGGT
CTGTGAGCTCTGCTGTTTGGGAGCTATTCTGGCCAGCAGAGGTAGCCTAGTCTGATTCGCTGATTCGCTGAT
ACAGAGAGTGTGGAGAACAGTGTAGGCTGGCTGTACAGGTAAGTGTGATCTGACAGCAGGCTCAGCCATAC
TCTTACTATCATGCGACGAGGGGCGCTGACATCTAGGACTTCAITATTCTAATTCAGGACCAAGCTGGAGTA
TGATCCTCACTCTGATTGGATGATCTGAGGAGAACAGGGGGGCGGTCTCGAAGTGGAAATAAATAGCGGCC
GCGTGGTACTTGCACCTATAATCCAGCACTTTGGGAGGACAGGCTGGGAGGATGCTTGGTCCAGAGATCA
AGACCAGCTGTGGAACATAACAGACCCGCTCTACTATTAAAAAAGTGAATAAATGATAATAT

FIGURE 60

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQKGKPGACW
MASRFSRVVLVIDALRFDAQPPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTTMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLTIAHFLGVDHCGHKHGPHHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPFNGNIGEVMAELFSGGEDSQPHSSALAAQASALHNAQ
QVSRFLHTYSAATQDQLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPFCPLLLTPVAWGLVGAIA
YAGLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRILA
VFFSDSFVVAEARATPFLGSGFILLVVQLHWEGQLLPKLLTMPRLGTSATNPNPRHNGAY
ALRLGIGLLLCRTLRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMLVP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLETKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLFLQSF
LLHLLAAGIPVTTGPFPTVPWQAVSAWALMATQTFYSTGHQPVFFAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEEP
LMMRLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLVMVKVFAPKFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAATTTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGGAAAGAGAATCCAGAAGACCTTCTGTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTCTTTCTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA
 GATTCTTTGTGCTGCTGAAAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGAT
 TCTAAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTTGATGGAAATTTTTGTGACTCTGAAGAAAACCGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAAACATACCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCG
 CAAACGTTACAGTACTCATACCCCTCAGCTCCAAGACTTAGACCCCTTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCTTGGTCGACTGGGATCCCC
 AAACCTGGCAGGCTGTGTATTCCCTTCGCTGTGTCAGCTTCGACCAGGATTCAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
 TATATGTGCAGATGAAAAACTGATGCCAACACTTCTTTTGCCTTTTGTTCCTGTGCAAAC
 AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGT
 TGTTCATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTTCAGG
 TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSIQGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNED
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSSSFDQDSEGCEPSEGDGLGEEGLLSRLYEAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTCTGGGCGCCACGTCTTGAGTACTGCGGAGCCCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTCTGGGCCTGCACTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGAGGTGCCGCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCC
CCAGCCCGGCCCTGCTGCGGACCACAGGCCCCCAAGGAGAAGCCGCCTGAGCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAATGTTAAGTACAAAAAAGAAAAAAGAAA

FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
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LLRLNGSAVLGPAVGLLRLPGRRAREPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
 CGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTGCGCGCTGGGCACGGTAG
 CAGGCGCGCCGCTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
 GGAATGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAAGTTTGGCGTTAACCACCTGGGTCACTTCTCTTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATTGTTGCTGG
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCCTACT
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
 CATCCATGGCTCCACCTTCTCCAGACCCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA
 GGTGGCCCGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGCTTAGAGGCTCCCTCTGTGA
 GGGAGCAGCCCCCTCCCGAGATTAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCTCCAG
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGC
 CTGCAAGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
 TGTGCACTTGCAGGCCAGCTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
 TCCGTGAAGAGCATGGGAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
 TGTGCATGCATGGTCTCTCTGAGCCTTGGTTTCTTACGAGTGAAGTGTCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
 GGTGTTTGGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAAGTGTCTATCCC
 GAGTTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGTACAGGACCTGGGA
 TTGCTGGGACTCCCACCTTCCATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAA
 TTGCTCATT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIIEEERVLDILINN
AGVMRCPHWTTEDGFEMQFGVNHLLGHFLLTNLLLDKLGKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
 CAGCGTGGCGCGCGCCTGGCGCCCAGCGCCGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTACTCTCATCAAACGCGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATCGCGCTGTCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGCTTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAAATAAGAGG
 ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
 TGAGGCTGTCTACAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAGACCCCTGGGTTCCAGCCCCACTCTCTACAGATCCCTAGCCTCTACTGTTCTTAT
 GAGACCAATTCCAACGCCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCAATCCACCTGGA
 GCCCTACATTGCTCTCTACCATGACTTTCGTAGTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTGAGTGGTGGCATCAGGGGAGAAAGCATTAAGAAGTGAG
 TACCGCATCAGCAAAAGTGCTTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCCTCAA
 CCACCGCATTTGCTGCCCTCACAGGCCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACCTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCAACAAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGCCACAGCCTTCATCTATGCCAACTCAGCGTGCTGTGGTTAGGA
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGCTGCTGGTGGGAGATAAGTGGGTGGCCAAACAGTGGATACATGAGTATGG
 ACAGGAATTCGCGAGACCCCTGCAGCTCCAGCCTGAAGACTGA**ACT**GTTGGCAGAGAGAAGC
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAGCTGGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCCTCGCAATCAGAGGC
 AAGGGAGAGGTTTGTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCCTGAGAGGAGAGTTTCTGG
 AGTTTCAGATACCTCTGTGGGAAACAGGACATCTCAACAGTCTCAGGTTTCGATGAGTGGGT
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCAGAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTTCTTTTCTTTTGTATGATGTTTTTTAACACAGTCATTA
 ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPLHQLTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCGCTCCCACCCCTAG
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
 CGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCCT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCCTCC
 TGGCTCCAGCCATCATCTCATCTCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTTTGGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
 ACTTCTGAACGACAACATTCGAAGAGGAATTGAGAATACTATGATGATCTGGACTTCAAA
 AACATCATGGACTTTGTTAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATTGTGTGGCTACAAAACATTCGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTATCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
 CTGGTTATCGGACAACACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCGGGTGGAGGACATCATCATGGAGCAC
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAATTAGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCTGTGTGTAGGTCCACGGCCTCTGCCCTC
 CCCAGGGAGCAGAGCCTGGGCCTCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT
 GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTCTCCAGGCCTGGGCTACAGGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTGGC
 CTCTTCTCAGCCTCCCAGGTGCCCTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGGCCCTA
 GTTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATCTTGCCCTTCCCCAACCAGTTTGTGTTAA
 TCAAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCAREFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAP
AIIILLLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGIEINYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

CAGGAGCGGGCCGAGAGACTCCAGCGTGCCAGGCTGGCATCCTGCACCTTGCTGCCCTCTGACACCTGGGAAGATGGCCGGCCGCTGGACCTTCACCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCCAAGCCACCCTCAGTCCCACCTGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAGCTGACACAGGAGCTGAAGGACCACAAGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCCTGGTGAACACAGTCCCTGAAGCACATCATCTGGCTGAAGGTGATCAGCATTAACATCCTCCAGCTGCAGGTGAAGGCCCTCGGCAATGACCAAGCAGCTGTGAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACAGCCCTTGTTCAAGACCATCTGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATTCGATGGACACCAGTGAAGTGGCCCCACC CGCTGGTCCCTCAGTGACTGTGCCACCAGCCA TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTCTGGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGCCAATCTAGTGAAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTCCTCAGCATTTAGCCGTCFGAGTTTGACCTTCTGTATCCTGCCATCAAGGTTGACACCATTACGCTCTACCTGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCTTGACAATGCCACCCTGGACAACATCCC GTTCAGCCTCATCGTGAGTCAAGGACCTGGTGAAAGCTGCAGTGGCTGTGCTGTCTTCCACAGAAGATTCATGGTCTGTGGACCTGTGCTCTCTGAGATGCCCATCGGCTGAAGTCAAGCATCGGCTGATCAATGAAAGGCTGCAGATTAAGCTGGGATCTCCAGAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT TTTTATAGACCAAGGCCATGCCAAGTGGCCAACTGATCGTGTGGAAGTGTTCCTGCCA GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGATGAAC TCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAGATCTGGGGTCCCAAGTGTCATTGGTG AAGGCCTTGGGATTCTGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTGGAAACCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGAAGGCTGGGTCCCAGTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAACACTTGCCCTGTGAAAAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNNATSILQQPLLSAM
REKPAGGIPVLGSLVNTVLKHHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGTIQLYL
GAKLLDSQGKVTKWFNNASAASLTMTPLDNIPFSLIVSQDVVKAABAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLTTPASLWKPPSSPVSQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGCTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTGGCGAGCTTCCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCGTCGCGCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAACTGCATAGACAGTGTGTCGTTTGAACGCAAGCTGATGAAGAATTCAGATCCTGGC
 AAATCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTGGCATGGTGGATTTTG
 CTGAAGGCTCTGATGATTTTCAGATGCTAAACATGAATTCAGCTCCAACCTTCATCAACTTT
 CTGCGAAAAGGGAACCCAAACGGGGTGATACATAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
 CAAATATGCTGGTCCCCCTATGTTGGGATTGCTTTTGGCTGTTATTTGGTGGACTTGTGTAT
 CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGACGCTTTGTG
 TTTTGTGCTTGTCTATGACATCTGGTCAAATGTGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGT
 GCTGAAACACACATTGTTCTTCTGTTTAATGGTGGAGTTACCTTAGGAATGGTCTTTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGAAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTCTATTTTAGATCTAAATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAGGTTCCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTGTATTAC
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAATTTGAAAA
 CTACTACTTTGTTTGTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCACTGTAT
 TTTATATTGCCTTATCCAAAGATGGGGAAGTAAGTCTGACCAGGTGTTCCACATATGCC
 TGTTCAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTGTGATGGTCTTCTGAAAAATG
 GAACACCATTCTTCAGAGCACAGCTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
 GCATATTTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTTACAGATTCATTCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAAATA
 TAGCTTAGTGCTAAAAATCAGTGTAACCTTATACATGGCCTAAAAATGTTTCTACAAATTAGAGT
 TTGTCACTTATTCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTGAGGATTCGAGACCATCCTGGCCACACATGGTGAACCCCGTCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GGAATCACTTGAACCTCAGGAGATGGAGGTTTCAGTGAGCCGAGATCACGCCACTGCATCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMWNTNKRPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLEFNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACCTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGCGGCTGGCCGGCGGCAGGCTCTCAGAACCGCTACCGGCGATGCTA
 CTGCTGTGGGTGTGGTGTGCGAGCCTTTGGCGCTGGCGGTACTGGCCCCGGGAGCGGGGA
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGTGGTGTGGTGTGGGAGCGGACTCCTTCGATG
 GAAGGTTAAACATTTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG
 ACACGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC
 AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAGGGTCTAG
 ATCCAAATTATACAACTGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
 GGGAAACTGGACTATACCTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA
 CTAAGTCAGAGTGATGGAAAGGGATTGGCAGAATACAGACAAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAATTACACTGAACCATTGTATTATTACTTGGGATTAATTTACACACCCC
 TTACCCTTCACCATCTTCTGGAGAAAAATTTGGATCTTCAACATTTACACATCTCTTTAT
 GGCTTGAAGAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTCAAGAAATG
 CACCTGTAGATTATTACTCTTCTTATACAAAAACCTGCACTGGAAGATTTACAAAAAAGA
 AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
 AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTCTATACTCTCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGGCCTACAAGTATCAAATG
 TGGTTTCTCTTGTGGATATTTACCTACCATGCTTGATATTGCTGGAATTCCTTGCCCTAG
 AACCTGAGTGGATACTCTTTGTTGCCGTATCATCAGAAACATTTAAGAAATGAACATAAAGT
 CAAAAACCTGCATCCACCCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA
 CCTACATGCTTCACTTAACCACTGGAATATATAGCCTATTCCGATGGTGCATCAATATTG
 CCTCAACTCTTTGATCTTTCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAATTTTCC
 AGAAATTACTTATCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCATAAAGTTTCTG
 CTTCTGTCCACAGTATAATAAAGAGCAGTTTATCAAGTGAAGCAAGATATAGGACAGAAT
 TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGGCAAGGAAGCAAGGAAGTA
 TGAAATGCAATTTGATCAGTGGCTTAAACCCCATATGAATCCAAGAGCAGTTTGAACAAAAA
 GTTTAAAAATAGTGTCTAGAGATACATATAATATATTACAAGATCATAATTATGTATTTT
 AAATGAACAGTTTTTAATAATTACCAAGTTTTTGGCCGGGCAAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAGCAGATCACAGGTCAAGAGATTGAGACCATCCTGGC
 CAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATAGCTGGGCGCGGTGGTGACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCGAGGAGATCGCTTGAACCCGGGAGGCAGCAG
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTCTG
 AAAAAATAAAAATAAAAATAATAATTAACAAATTTTTCATTATTTGTAAGAATGTAGTG
 TATTTTAAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAATGGTTATTATTTA
 GGCCTTTGTACAATTTCTAACAATTTAGTGGAGATCAAAAGGATTGAAGCAAAATCATGTA
 ACAGTTATGTTCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATATAAAT
 AGTTGTATGTGAGCATTTGATGGTGAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSDFGRLLTFHFGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTO
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVVIYLG LNLPHFYPSPPSSGENFGSSTFHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEI ILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGP GIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSI INYPKVSASVHQYKNEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
 GGTGGCCATGCTGCTCCCGAGCTGAAAAACAAGTTCTTATGTGCGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCAG
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
 ATCCTTGGAGGCCTCCTGGGATTCACTCTGTGCGCTGGAATCTTCATGGGATCCTACGGGA
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGAGAGGCTCTTTACTTTGG
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTTACAGCCTGACAGGGT
 ATGTG**TGA**AAGAACAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCCTGGATCGTGTGAGAAAGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
 CAGGTGGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
 CCCTGCCCTAAGTCCCAACCTCAACTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCAAAACCCACTAATCACATCCACTG
 ACTGACCCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCC
 AGACTAATTTGTGCATGAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYILGLLGLLGLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRFGQPPKVKSEFNSSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCAC TGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCTTTGGCCTCACAAACGATTTTGTTG
TGAAGCTGAAGGTTCAAGGTGTGAATCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTTGAGAGACATAGAAAGAAAAACAACCTTCAC TAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGTTTTC CAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDVFVVKLVQGVNSQCHSSPISKCESRRRFP

Signal peptide:

amino acids 1-25

Downloaded from www.jstor.org

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAAGTGCGA
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTAATAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCTGGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCCCT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TCGCGGGAGGCTTCCCGCGCCGGCCGCGTCCCGCCCGCTCCCGGCGACAGAAAGTTCCCTCT
 GCGCGTCCGACGGCGCAGCATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCGAAGCTCACCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCAGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCATCCGCAACCTCACGTTCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG
 GATAGCGGCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACCTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAGATGCACCATCCAACCTGTGTGGTGT
 ACCCATCTCTCTCCAGGATAGTGAACATCACGGCTGCAGCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAACCC
 CCGGCTTTGAAGCCTCACCACTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCCAGCAC
 CCCCCGTCTCTCCAGGCCCGGAGACGCTTCTTCCCATCCCTGGACCTGTCCCTGACT
 CTCCAAACCTTTGAGGTCTCTAGCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCCTCGGCCCTGGTTC
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGTGCTGAG
 ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACAGGGCACGGTG
 GAGAGACTTCTCCCCGTGGCCGCTTGGCTCCCCCGTTTTGCCCGAGGCTGCTCTTCTGTC
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCACTGGCCATCGCC
 ACCTTCCCCAGCTGCCTCTACCAGAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGGCTGCATTCAGTCCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCCACCCACTGGAGATGGTGTGCTGAGGAGGTGGGTGGGGCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCCCTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLLVYKQQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDVPDPSNFVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCTTTCGTCTCTCCATCTCTCCCTCCT
TTCCCGCGTCTCTTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCTC
TTTCTGCCCACCGCTGCTTCTTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
GGTCTGTGGGTGATCTGTGGCCCCGTGTCCTCCGTGTCTTTTCGTCTCCCTTCTCCTCCGA
CTCCGCTCCCGGACCAGCGGCCGTGACCTTGGGGAAGAGTGGTTCCTCCGAGGTGAGGGTCTCT
TCCTCCTTGTCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT
TGGAGCCACAAGGCCTGATGTA CTGCTGCGCTGTACCTGCTCAGAGGGCGGCCATGTGAGT
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
CTGTCCCAAGTGTGGAACCTCACCTCCCTCTGGACTCCGGGCCCCACCAAAGTCTTGCC
AGCACACGGGAGCATGTACCAACAGCGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGGGGCCAGATCTACTGCGGCCTCAC
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCCTGCCAGACTCTGTCTGCCAAGCCT
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCTGCTCCATGGGGT
AGACATCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
CCCCACTGGCCTCAGCGCCCCCTGTGAGCTTATCCCTCGCCACTTCAGACCCAAGGGAGCAG
GCAGCACAACTGTCAAGATCGTCTTGAAGGAGAAAATAAGAAAGCCTGTGTGCATGGCGGG
AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCGTGCTTTCGGCCCCCTTGCCCTG
CATCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
ACCCCTGCCGTCAACCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCCAGAGGACAAA
GCAGACCTTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTCT
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGCTCGCTTTGCCCTGGAACACGAGG
CTCTGGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG
AGAGTGGAAGTACCTGCCCCAAGGCCACAGCCAGAAATCTTCCACTTGACTCAGATCAAGA
AAGTCAGGAAGCAAGACTTCCAGAAAGAGCAGCAGACTCCGACTGCTCGCTGGCCCCCAG
GAAGGTCACTGGAACGTCTTCTAGGCCAGCAGCTGGAGCTGAGGCTCAGCGCCAGTCCAGA
CAAAGTGACCAAGACATAACAAGACCTTAAACAGTGTGAGATGAGCTGTATAATTGTTGTT
ATTATATATTAATAAATAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARAPDMFCLFHGKRYS PGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVCSCCTEGQIYCGLTTCPEFGCPAPLPLPDSCCQACKDEASEQSDDEED
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFPRK GAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGLPCILCTCEDGRQDCQRVTCPT EYPCRHP EKVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

[illegible]

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNNMVGEGGASGRSP

Signal peptide:

amino acids 1-18

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89
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95
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97
98
99
100

[illegible]

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MGPSTPLLLILFLLSWGFLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVL DGTQNDTAFVFPRL
RDFTLAMAARKASRVRVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDTQ
QWDTPCPRENAEAAFVICGTYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCTCCGCTCACGCAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
 CCGTCACCTCTCCTGTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
 CTCTCATGCTCAGTTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTCTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTTCTTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAAATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCCATCACGGGATATGTT
 GATAGAGACATCCAGTACTCTGTGAGTCTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
 GAAAGGTCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTGTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAAATTCAGTGAAAAATCCAGCGGAACTGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG
 GCGCTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCAGGACCCACCTACAAAAATAGGGGTCTTCTTGAGCTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTATACCTGACATGTCCGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTATAATGAGCAAAATGAACTCCC
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAGAGGCCCTTGGCAAAGGCCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCAGCCCTTCTCCCCAGGG
 GTGAAATGTAGGATGAATCACATCCACATTTCTTTTAGGGATTAAGGTCTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCGGCCAAGGTGGCTTCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFCFLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGDLSTDSRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL
PDHGYWVLRNLNGEHLVFTLNPRFISVFPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPESTNSSESSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
 CATGAGGAGCCTGCCGAGCCTGGGCGGCCCTGCCCTGTTGTGCTGCGCGCCGCCGCGCGCCG
 CCGTCGCCCTCAGCCGCTCGGCGGGGAATGTACCAGGTGGCGGCGGGCCGCGGGGAGGTG
 GACGCGTGCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTTAGGGCGACGGC
 TCCCAGGCCCCAGGCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTC
 ACCACCTTTCAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCATTC
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTCGACGACCACTGGCCCCG
 CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCGGACCCCGACCCCG
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCTCTCTCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGCGAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACC
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTAAGCAACAGAGGGTGGAACTGAAGTTTAT
 TTTATTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTACAAAATATTTATATACCTTTTATCTCTACTTTTATATGT
 TATATTTAATGTGAGGTTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAG
 AGTCGCAATTTTTCTTGGGATAATTTCTGTAATTTTCATGGGAAAAAATTATTGAAGAA
 AAATCTGCTTTCTGGAAGGGCTTTAGGCGATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
 ATCAAAATTTACATTTGTTTCTTTGGACATCTAAAGCTTAACTGGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGCCAAAAG
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTGAGGTAATTTAATCTAGTGA
 ATAATGTACTGTTATCTAAGCATTGCTTGTACTGCACTGAAAGTAATTTATCTTTGACCT
 TATGTGAGGCACCTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGTTTATCTCAGTGTAACCTGGGTATAACCCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTGTTCTTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTTGTGTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAATGTTTAAAG
 ACTTTTAGCTCCTTGACAAAGAGTGCTTTATACTTTAGCACTAAATATTTAAATGCTTTA
 TAAATGATATTATACCTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGTCTCTACTAAA
 AATACAAACAAATAGCTGGGCGTGGTGGCACACACCTGTAGTCCAGCTACTCGGAGGCT
 GAGGAGGAGAATCGGTTGAACCCGGGAGGTGAGGTTGCACTGAGCTGAGATCGGCCACT
 GCACCTCCAGCCTGGTGAAGAGGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGLLALLCCAAAAAASASAAGNVTTGGGAAGQVDASPGPGLRGEP SHPFFRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSSTTFQAPLGPSP TTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAP TTPVATTVPAPTTPRTPTPDLPSSSSSVLPTPPATEAPS
SPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLN YTSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGC GGTTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGT CATGGACCTGATAAAGCGAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTCA**CAGTAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAAFLALVSVPRQA~~V~~WLGR~~L~~DPEQL~~L~~GPWYVLAVASREKGFAMEKDMKNVVG~~V~~VVT
LTPENNLRTLSSQHGLGGCDQSVMDLIK~~R~~NSG~~W~~VFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGACAGGAAGGCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGTGGAATTTACCTGGCCAGTAGTTCATGGCTACTGGTTCCGGGAAGGGCCAAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
 GCACCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTGAGCCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGAT**TGA**GAAACTGCAGAGACTCACCTGATTGAGGGATCAGAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETDRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVFWACEQGTTPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTTNKTVHLNVSYPPQNLMTMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRGSSASQGPLEPWAEDSPPDQPPASARSSVGEGLQYA
SLSFQMVKPDWSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AAGACCCTGTTCTCTG
 GGTGTCACGCTCGGCCTGGCCGCTGCCCTGTCTTCACCCTGGAGGAGGAGGATATCACAGG
 GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCCAGGA
 AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
 ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
 ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT
 ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
 AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
 ACTCTCGGAGGAGGACATTTTCAGCCCTGCAGACGGGAAGCTGCGTTCCTCGAACAC**TAGG**
 CAGCCCCCGGGTCTGCACCTCCAGAGCCACCCCTACCACCAGACACAGAGCCCGGACCACCT
 GGACCTACCCTCCAGCCATGACCCTTCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT
 TTTCCCCCAA

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:**Signal peptide:**

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAAGGGGAGAGACCAGGATCATCAAGGGGTTGAG
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTCGAGAAGACGCGGCTACTCTGTGG
 GCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTTAGCACCA
 GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCCTCCATTTCCACTTGGTGTTTGGTTCTGTTCACTCTGTAAAT
 AAGAAAACCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSTITW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRCANITIIIEHQKCNAYPGNITDTM
VCASVQEGGKDSCQGDSSGGLVLCNQSLQGIISWGQDPCAITRKPVGYYTKVCKYVDWIQETMKNN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

GAGCAGTGTCTGCTGGAGCCGATGCCCCAAAAACCATGCATTTCTTATTAGATTCAATTGTTTCTTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGACCCGAAGAA GTGAAAAATAGAAGTTTTGCATCGTCCAGAAAAGTCTCTAAGACAAGCAAGAAGGGAGACCT ACTAAATGCCCATTTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGAGCCGGA CACAAAATGAAGGCCACCCCAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG AGATTGAACCTTTATGCTGTGACCAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTTAAGA AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT GAACATAAGTCATATTTGTATTTCTACTTTTTTTTTTGTAGCTATTTACTGTACTTTATGTATA AAACTAAGTCACTTTTCTCAAAGTGTATTTGTATTTTCCCTATGAGAGATATTTTGA TCTCCCCAATACATTGATTTTGGTATAAATAATGTAGGCTGTTTTGCAAACTTAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGKRRVVI PPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDDHGDGFISPKYENVYQHDEL

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Important features:**Endoplasmic reticulum targeting sequence.**

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTGAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGP~~LL~~LPGLCFLLSLFGAVTQKTKTSCAKCPPNASC~~VNN~~THCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSR~~L~~

Signal peptide:

amino acids 1-18

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FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGGCAGAGGTGGGGGGCAC
 AGGGAAAGGGTGACCTCTGAGATTTCCCTTTTCCCCAGACTTTGGAAGTGACCCACCATGG
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGGCGTAACACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
 CAGCCTGCGCTGCGGGGGTGCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC
 CCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGCTCTCAGGCTGGGGC
 ATCACCACCCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCGGGGCAGGATGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGG
 GTCCTTCAAGGTCTGGTGTCTGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGATGATCATGAGGAACAACTGAC
 CTGTTTCTCCACCTCACCCCAACCCCTTAACCTGGGTACCCCTCGGCCCTCAGAGCACC
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACCTCTTGGAACCT
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQATPKFI FNGTECGRNSQPWQVGLFEGTSLRCGGVLI DHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSV
QPLPLPNDCATAGTECHVSGWGITNHPNPFDDLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPQGDACQDGGGLVCGGVLOGLVSWGSGVPCGDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

CHILDREN'S RIGHTS

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGAAGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCCTCCAGAAAA
 GCTCAGAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
 TGATGTCCTTTAAAGAGGATGATGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTGA
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTCATTGAGGGTTTGTGTTGTTT
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGAATCC
 TGAGCCTTGGGTCCCTCCCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG
 ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGCGAGGAGGCTTCCAGCCTGTGTTCCC
 CTCACCTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAAGGGCCTCTTTGCGGTTTTCCTTGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCCCTCCAGTCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
 GGGTTTGGGGGAAAGGTGAGCTCAGTGTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTTGCTGACCCCAATCTGCTTGAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSPKFVGPPPERDIASLP

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FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGCAACACATGCGCCCCGGGTGGGCAGGGGTGCGCGCCGCGCTGCGCGCC
CGCTTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCCTCCAGCGCTGCGCTGGCC
CACCAGTGTAACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTCCGCGCGGTTT
CTCGGGGACATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGTGGGCTCAAGAACCTCCGAGTCTTGATCTTGGAGACACACAGGT
CAGCGTCATCGAGAGAGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAATAACGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCACCGATGT
GAAGAACCTGCAACTGGACAACAACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGAGTTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCTCTGGTCACGAGC
TTCAACCACATGCCGAAGATCCGAACCTGCGGCTCCACTCCAACCACCTCTACTGCGACTG
CCACTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGACAGTTGGCCAGTTTACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCGAGAAGAAGGAGTACGTG
TGCCGAGCCCCCACTCGGAGGCCCATCTGCAATGCCAACCCTCATCTCCTGCCCTTCCGCC
CTGCACGTGCGACAATAACATCTGGACTGTGAGGAAAGGGCTTGATGGAGATCCTTGCCA
ACTTGGCGGAGGGCATCGTCGAAATACGCTAGAACAAGAACTCCATCAAAGCCATCCCTGCA
GGAGCCTTCAACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCCGA
TATTGCTCCAGATGCTTCCAGGGCTGAAATCACTCACATCAGTCGTCTGTGTTGGGAACA
AGATCACCAGGATTGCCAAGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAGATCAACTGCCTGCGGGTGAAACACGTTTCAAGGACCTGCAAGACCTCAACT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCCGCCCTGCGAGT
CCATCCAGACATCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGACAACCCCATCGAGACAAGCGGGGCCGTGCGAGCAGCCCCGCCGCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTCAAGAGCGAGTGCTTCAAGACCTCGTGTGCCCGAGAAGTGTGCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACTCCC
TGAATATGTCACCGACTGCGACTGAATGACAAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCGAGGAGTGATGCTGACAGGGAACCACT
GGAGACCGTGACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA
TAACTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCAACCAGCTTGTCTCCCT
GTCACCATAAACCTCCTGTCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGGGCGGATCGTCAGTGGGAACCTTAGGTGCCAGAAGCCATTTTCTC
AAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
TAGTGCAGCTGAGCCGCGCTGCCCGGAGCAGTGACCTGTATGGAGACAGTGGTGGAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCGAGGCGATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAACCACTTAACAGCCGTGCCAGAGAGCTGTCCGCGCTCCGACACCTTGACGT
TATTGACTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGCTGAGGTGCATCCCGTCCACGCTTCAAC
GGGCTGCGGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGGCTTCTGAGG
CTCCTTCAACACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCACTCACTGTG
ACTGCAGTCTTCGGTGGCTTCTCGGAGTGGGTGAAGGCGGGGTACAAGGAGCTTGGCATGCC
CGCTGAGTACGCCCTGAGCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCCGCTT
CCAGTGCAAGGGCCAGTGACATCAACATTTGGGCAAAATGCATGCTGCTTCCAGCTTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGGTGTACCGTGTGCTGCCCC

TACAGCTACAAGGGCAAGGACTGCACCTGTGCCATCAACACCTGCATCCAGAACCCTGTCA
GCATGTGAGGACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGTGCTCTGCCCTCT
TGGCCTTTTGGGGGGACGGGTGTGAGATCAACCCAGATGACTGTGAGGACAACTGCA
ACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCTTAAC
ACAGGTGAGCTATCGCAGAGGTGATTGACCACTGTGTGCTTGAGTGAACCTCTGT
AGGCCAAGTGCACTCCCTCTGGACAAGGATTCAGCTGCGAGTGTCTCCCTGGCTACA
CGCTCTGTGAGACAGCAATGATGACTGTGTGGCCCAAGTGTCCCGCAGCGGGCCAGT
CTGGGACACAATCAATGGCTACACATGCACCTGCCCGCCAGGGCTTCAGTGACCTTCT
AACACCCCCACCCATGGTCTTACTGTGAGACCAGCCCATGCGACCACTACGAGTGCC
GGGGCCAGTGCATCGTGGTGCGACAGGAGGCCACCTGCCCTGCCCAACAGGGCTT
CCCGACATGCGAGAAGCTCATCACTGTCAACTCTGTGGGCAAGAAGCTCTCACTG
CCTCCGCCAAGTGTCCGACCCCAAGCAACATCTCCCTGCGAGTGTGCCATGCAAGG
GGCATCTTTCTTACAAGGAGACAATGACCCCTTGGCAGCTGGAGCTGTACCGAGG
CGCGCTGGTCTTAGTGACAGCCTGAGTTCCTCTCAACCACTGACAGTGTGAGGACAG
ATGATGGGCGAGTTTTCAGAGTGTGGAGTGCTGAGCTTAACACAGACCTGAACCT
GACAAAGGAATCTCAAGAGCCTGGGAGAGTCTCAGAAGCGCAGCAGTGGGCATCA
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCTTGGCGCAGG
ACGGCCCTGTAGGCGGCTTCCACGGATGATCCATGAGTGCGCATCAACACGACG
GACTTCAAGGCTCTCCCAACAGTCCCTGGGGGTGTCAACAGGCTCAAGTCTCGAC
GTGCAAGCAGCGCTGTGCCCTCGTGGAGAAGGACAGCGTGGTGTGCGAGTGC
CTGGACCGGCCCTCTGCGACAGGAGGCGGCCCTGCCCTGCCCAAGATGCCAC
CATGGAAATGTGTGGAACCTGGGACCTATACATGTGCAAGTGTGCCGAGGCT
GGACTGTGTGACAAAGAATGATCTGCCAATGCTGTGACGCTTCAAGTGTCCACAT
GGCAGTGCCACATCTCAGACAAAGGGAGCGCTACTGCTGTGCCAGCGGCTTGA
GAGCACTGCCAACAGAGAATCCGTGCTGGGACAAGTAGTCCGAGAGGTGATCCGCG
GAAAGGTTATGCATCATGTGCGACAGCCTCCAAGTGCCCTATGGAATGTCTGTGGG
GTGGGCCCCAGTGCTGCGAGCCACCCGACAGCGCGGCAAGATACGTTCTCGTGGC
CAGGGCTCTCGTTTGTAGAAGAGGTGGAGAGACTTAGAGTGGCGTGCTCGGTGTT
CTAGCGCCCTCGCCGCTGCTGCCACCTCTCGGACTCCGAGCTTGATGGAGTGTGG
ATGTGGGACCCCTGGTGATTGAGCATGAAGGAATGAAGCTGGAGGAAGGTAAGAAGA
AGAGAATTATTAAGTATATTGTAAAATAAACAAAAATAGAACCTAAAAA
AAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKQLVL
 PELLFQSTPKLRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
 TLNNNNISRI LVT SFNHMPKIRTLRLHSHLYCDCHLAWLSDWLQRRTVGQFTLCMA PVHL
 RGFNVADVQKKEYVC PAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAIPAGAFTQYKKLRIDISKNQISDIAPDAFQGLSKLSTSLVLYGNKITEIAK
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTIISKGLFAPLQSIQTLHL
 AQNPFCVDCHLKWLADYLDQNPDIETSGARCSSPRRLANKRISQIKSKKFRCSGSEYDRSFS
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLRNDNEVSVLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
 SNTDFAGLSSVRLLSLYDNRIITITPGAF TTLVSLSTINLLSNPFNCNCHLAWLGKWLRRR
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGRL
 ALPRGMPKDVTELYLEGHNLTA VPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
 SYNRLRCIPVHAFNGRLSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHR FQCKGPVDINIVAKNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGDCTVPINTC IQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR
 CEINPDCCEDNDCENNATCVDGINNYVICIPPNYTGELCDEVIDHCVP ELNLCQHEAKCIP L
 DKGFSCCEVPGYSGKLCETDND CVAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPPMV
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP
 QANISLQVATDKDNGILLYKGDN DPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS
 VELVTNLQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
 HGCIEHVRINNELQDFKALPPQSLGVS PGCKSCTVCKHGLCRSVEKDSV VCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEYGGDLCDKNDSANACSAFKCHHGQCHISD
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVI RRQKGYASCATASKVPIMECRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGAAACTGGATCTGCATGCCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCTTGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTTCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCCT**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAATGCCTGTGTATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAACCTTGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

115/249

FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAACCTGTACATGGCTCCC
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTACCTTGGTGTCTGCCTGTATCCCACTGTTT
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCAGATCTGCTTCTCAC
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTATGTCTCTATCCATCTCTAAATGTACCAG
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAAATGGTCCAAC
 AGTCCGACCTTGCCAGTATGTGACCTTCTTGAGTCTTCTCAGACAAACAGAAAATCTCC
 CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCTTGGAGT
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCCTTCTCAGAAGCA
 ATAGAAAAGTTTATCCGTGAACCTTCCTTAAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTAT**ATA**TCAGATTGTTTTTAAGATCTCCATTAATGTCACTTTTATGGATTGTAGACC
 CAGTTTTGAAACCAAAAAAGAACTAGAACTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
 AACCATGTCTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
 TCATTCCATGTTTACGAGAGTATTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
 TAAATTTGAATGATACTGTGCCTTAATTGGTTTTCTAGTTTAAAGTGTGTATCATTATCAA
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCAGATTCAAT
 CCACCGAAGTGTTCACTGTCTGTGTAGGAATTTTGTGTGCTGCTTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAAATTTGTATTTTGCACACTGAGATATAA
 TAAAAGGTGTTTATCATAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLARRRKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGR LTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSC TCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFI REPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATG**TTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCCTGGT
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCCAATAAGACATCGGACCCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATATGAGGAAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTGGCT
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTCAC
 TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAACCACTCTGAA
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAACTGTTGAACTGCCA
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATATT
 CCTAGAGAGACCTCGTCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCTCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCAGAGTTGAGGTTTGCATATATGGTGACCACA
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
 AT**TAA**AATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
 AAATCTATGTTGAATCCTTTTATAAACCAAGTATCACTTTGTAATATAACACCTATTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS LGTVDLKQHINPNKTSDFETMLKSLRLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGFLDGS LDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLT TSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVL
QDPNTWPSPHKFD PDRFDDELVMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
GACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTTCGTCATCACCTTATTCTGGTCCCGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACACCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTACCGTCTTTGGGCTGAAA
AAGAAACCTTCTTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCTTGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGACA
ATTAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
EMALFVTVFGLKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

121/249

FIGURE 121

TCCCGGACCTGCCGCCCTGCCACTATGTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGCTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCACGGGTGC
CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC
CTGCTGATCCGACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

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FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT
 GACTCGTGCTGCTTCGTGTTCTCGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCTCCCGGCTCAGAGGACCTTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
 CGGGTGCTCGGAAGCGGGCCACATCTCACCTAAGTCCGCCCCATGGCCAATTCCACTCT
 CCTAGGGTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAATCTTTGGCTGGGGCGACTTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCT
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
 TGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC
 AGGAGACCATCTGGACACCGGGCAGGGGAAGGGGTGGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCCAAGTG
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTCATCAGTGTGCACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGC
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
 GCTGATGGCACCCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC
 ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGGGCCGAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGAGCAGGAAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVCPCDYNVHSDTPY
YPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
GGCAGGGCTGATTCCTTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
TGGTGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGACAGCGTGTGACCTAGCCGCTAG
CATCTTCCCAGACACCGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
GGCTGCGGCTGCCACACGGCTCACC**ATG**GGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
GCCGTGCTGCTGGTCCCTACGCTGCCGGGGCTGCCGCTCTGGGCACAGAACGACACGGAGCC
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
GCTCCTCTTCTCCCCGCTGGGGATATCGGTCGGGCGGCCAACTCCAAGTGCCTTCTCG
GCGGTGCGGAGCACCACACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
CGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTGGAGTCTGTCTTTGTAGCACCAA
GAAAGGAATTTACAGTTTCAGTTTTACAGTGATTAAGTCTACCAGAGCCAACTATCCAG
GTTAACTTGTATGTTAAATGGAAAACCAAGTAATATCTGCTTTCGCGGGGACAAAGATGTTAC
TCGTGAAGCTGCCACGAATGGTGTCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
AACTGGAGAAAGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTTCTGGCTTTCTGGTG
TTCCCCCTA**TAG**GATTCAATTTCTCCATGATGTTATCCAGGTGAGGGATGACCCACTCCTG
AGTTATTGGAAGATCATTTTTTTCATATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
ACAGTCAAAGCTGTCTGCAAGACTTATTTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
TACAGATGTGGAATTTTATTTGTTTAGTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA
AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAGAAGCTGTATACTG
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTCTTGTA
AAAAGTTGGATTTTTTTTTTTCAGTAACGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
TGGCTTGCCACAAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAA
GAATGCTTCATAGTTGATTTTTAATGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
TTCTAAGAAAGAAGATAGATCATAAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCC**TCCGAGGGAAATCTTATACTTTTATTGC**
TCAACTTTAATAAAAATGATTGATAATAACCAGTTTATTAAAAACCTAAGGTTTTTTTTTT
TCCGTAGACATGACCACTTTATTAAGTGGTGGTGGGATGCTGTTGTTCTAATTATACCTAT
TTTTCAAGGCTTCTGTTGATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTAGTGCAATAT
CTTGCTTTTTGTATAGGTCATATGAATTCATAAAATATTTATGTCTGTTATAGAATAAAGA
TTAATATATGTTAAAAAA

FIGURE 126

MGSGRRALSAPPAVLLVLTLPGLPVWAQNDTEPIVLEGGKCLVVCDSNPATDSKGSSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFAVRKGIYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

127/249

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCGCTGCGCTC
 GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
 TTTCTTCTGGTTGGTGCTCTACTGATTTCTGTCCTTGTTTGGTTCATGGCAAGAGTCATTA
 TTGACAACAAAGATGGACCAACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
 TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
 GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
 TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
 CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTTCATGAC
 GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
 AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
 ATAAGTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCTATGGGCAC
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
 ACAAGAACTTTCTTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA
 ACCGCAGACTACATCTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
 GTGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIATFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLPGPTVGIHGDSPPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQSR

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACGACGCGCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCAGTTCGCTCTGGGCTTGCCTTCT
TGTGTCTCTTGGTGGCTCGGTGCAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGCTCTCGCAAGAAAGACGCCG
AGTTTGGAGCGCACTACGTGGACAGGTCAAAGAGAGTGGTCAACATCTACACCTCTCAACCATCTGTACCC
GCCAACAGGACAGAGGGCGTGGCTGTGTCTGTGAACGCTCCTGAACAGCAGAGGGGGCGCGTGTCTGTTTGTGG
TCCCGCAGAAAGGAGGCTGTGGTGTCTTCCAGTGCCTTAATCCTGCGAGGGATTTTTCAGCGCAAGTACCTCT
ACCAAAAGTGGAAAGCAACCTGTGTGTCAGCCCCCACCAGAATGAGTCGGAGATTCAGTCTCTTACGTGGATG
TGTCCACCTCTCACCAGTCAACACCACATACCAGTCCGGGTGAGCGCGATGGAGCATTTTGTCTCAGGACT
GGGAGCAGTTGAGCTTCAATACCACAGCAGCAGACGCCAGTACTTCAAGTATGAGTTCCCTGAAGGGCTGGACT
CGTAATTGTCAAGTGAACCTCCAACAGGCTTCCCTGCTCAGTCTCTCATTCAAGATGTGCTGTCTCTCTG
TCTATGACCTGGACAAACAGTACGCTTCTATCGGCATGTACCAGACGATGACCAAGAAAGCGGCCATCACCGTAC
AGCGCAAGAGACTTCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGCAAGACCAAGCTCGGGGGCT
CCCTGCTTTTACCCCTTCGCAGAAAGTGAACCGGTGATCAAGGGCACCGCCAGAAAAACCTGTGCTGCTGTG
TGTCTCAAGCAGTCACGCTCGAGGCATACGTCAGTGGGATGCTCTTTTGCCTGGGTATATTCTCTCTTTTACC
TGCTGACCGTCTCTGCTGGCTGCTGGGAGAACTGGAGGCAGAAAGAACCCCTGCTGTGGCCATTGACCGAG
CCTGCCCAAGAGCGGTCAACCTCGAGTCTGGCTGATTCTTTCTGCGAGTTCCCTTATGAGGGTTACAAC
ATGGCTCCTTTGAGAAATGTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCATTGGGACCTCTCTTACG
GTTACCAAGGGCGCTCCTTTGAACCTTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
ACTACGACACATTGACCGACATCGATTCTCGCAAGAAATGTCATTGCGCAAGCAATACCTCTATGTGCTGACC
TGCACGGAGAAAGCGGTGTTCTGGGAAAAAGTACAGATCTACTTCTGGAACATTGGCCACATTGCTGTCT
TCTATGCCCTTCTGTGGTGCAGCTGGTGTACCTACAGAGCGTGGTGAATGTACAGGAATCAGACATCT
GCTACTACACTTCTCTCGCCGCCACCCACTGGGCAATCTCAGCGCTTCAACAACTCCTCAACAACTGGGGT
ACATCTGCTGGGGCTGCTTTTCTGCTCATCTCTGCAACGGGAGATCAACCAACCGGGCCCTGCTGCGCA
ATGACCTCTGTGCCCTGGAATGGGATCCCAACACTTGGGCTTTTCTAGCCATGGCAGACCTGATGA
TGGAGGGGCTGCTCAGTGTGCTGCTATCTGTGTGCGCCAACTATACCAATTTCCAGTTTGAACATCTGTTCTATGT
ACATGATCGCGGACTGCTGATCTGAAGCTCTACAGAAAGGGCACCCGACATCAACCGCAGCGCTCAGTG
CCTACGCGCTGCTGGCCATTGCTCATCTTCTCTCTGCTGCTGGGCTGGTCTTTGGSCAAGGAAACACGGCGTTCT
GGATCGTCTTCTCATCATTTCAATCATCGCCACCGCTGCTCCTCAGCAGCGAGCTCATATTACATGGGCGGGTGA
AATGAGACTGGGGATCTCGCGCGCATCTCCACGTGCTCTACACAGACTCATCGGCAAGTGCAGCGGGCGCG
TCTACGTGGACCGCATGGTGTGCTGCTGATGGGCAAGCTCATCACTGGTCCGTGGCTGCTATGGGCTTATCA
TGGCGCCCAATGATTTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTGGCTTTATCA
TCTATCATGAAGCTCCGAGTGGGAGAGGATCAAGCTCATCCOCTGCTCTGCATCGTTTGAACCTCCGTGGTCT
GGGCTTCGCGCTCTCTTCTTCTTCCAGGGACTCAGCACTGGCAGAAAAACCCCTGCAGAGTGGAGGAGCACA
ACCGGGACTGATCTCTCTGACTTCTTTGACGACACGACATCTGGCAGTCTCTCTCTCTCCATCGCCATGTTCG
GTCCTTCTGGTGTGTGTGACACTGGATGACGACCTGGATCTGTGACGCGGACCAAGATCTATGTCTTAGC
AGGAGTGGGCGCTTCGCTTCACTCAAGGGGCGCTGAGCTCCTTTGTGTCTAGACCGGCTGACTCTGTCTGTGT
GTGGGATGAGTCCAGCAGCTGCCAGCACTGGATGGCAGCAGGACCGAGTCTGACTTAGGCTTGGCT
GGGACAGCCATGGGTTGGCATGGAACCTTGCAGCTGCCCTCTGCCAGGAGCAGGCTGCTCCCTGGAACCCCT
AGATGTTGGCCAAATGCTGCTTCTCTCAGTGTGGGCTTCCATGGGCGCTTGTCTTGGCTCTCATTT
GCTCCTTTGCCAAGGAAGGATGGAAGGGACACCTCCCATTTTATGCTTGCATTTTGGCGTCTCTCTCC
ACAACTGCCAGCTGGGACCTAAGGCTCTCTTTTCTCCCACTCCCACTCAGGGGCTAGTCTGGGGCGTGA
ATCTCTGCTGTATCAGGCGCCAGTCTCTTTTGGGCTGTCCTGGCTGCCATCACTGCCATTCCAGTCAAGC
AGGATGGATGGGGGTATGAGATTTTGGGGGTTGGCCAGTGTGGCCAGATTTGGTGTCAAGGCTCGAAGGG
CCTGGGCGAGTGCATTTCTTCTCCCTTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATCGCTCAGCCAAAT
TGAGAACCGCTTCTGATTCAAGAGCTGAATCAGAGGTCACTCTCTCATCCATCAGCTCCAGACTGATGCC
AGCAGCAGGACTGAGGGGAGAGGCGCTCACCCCTTCCCTTCTTCTTCCAGGCGCTTAGTCTTGCCAAACCC
AGCTGTGGCTTCTCAGTGCCATTGACACTGCCAAGAAATGDCAGGGGCAAGAGGAGGATGATACAGGTTACG
CCCTGTCTGCTCTCAGCTGTGGGCGCCAGTGCCTACTCTAGAAAGGGGCTCAGGAAGGAGTGTGCTGTTT
CCGTTACTGTCGCCACTTAGCTGCTCTAGGACCCAGGCTGGCTTCAAGTTCCGTCAGTTCTTCAAGCA
AGTTCTGTGTAGCTATGACACACATCACTATAAACCTTGGAGTTTACAAAGAAATGCCCCAGGCTTGGGCA
CCTGGCACCTGGTCTGCTTGAATCCCTTCTGCCACCTGGTCCACCGAGTCTGAGGATGGGGAGCTCAGG
CGGGGCTCTGCTTGGGATGGGAATGTTTCTCCAAACTTGTTTTATAGCTCTGCTTGAAGGGCTGGG
AGATGAGTGGGTCTGGATGTTTCTCAGAGCTCTCATGCTATGGTTGCAATTCGTTTCTATGAATGAAT
TGCATTCAATAAACACCGACTCAAAAAA

FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPELLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFFYVDVSTLSPVNTTYQLRVSRMDDFVLRGTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVFIGMYQTMTKKAATVQRKDFPSNSFYVVVV
VKTEDQACGGSPLFPYPFAEDFVDQGHQRKTLVLSVQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVADRACFESGHPRLVADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDSL SYGQGRSFEPVGT RPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVL RKKYQIYFNWNIATIAVFYALPVVQLVITYQTVNVNVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKNTAFWIVFESIHHIATLLSTQLYYMGRWKLDSGIFRRILHVLVYTDICIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

FIGURE 132

MVPAWLWLLCVSVQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRRLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSMDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSI IESTWVSLEPIHLAE
 NLKVLYPHHMAQVHVHSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAQYLLQVRAQN
 SHGEDYAAPLELHVLMVDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVGEGRAQVQDPTSGSVTLGVPLRAGQNIILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLQGAQPGDITYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRQLTNGSHAYLT LALHWVEPREHIIPVVVSHNAQMWQLLVIVCRCNV
 EGQCMRKVGRMGMPPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTCAATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTGCTGTCAGTCTGCAGGCATTTAAATCCTTCTCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
 CTTACCAATCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGGAAAGGCGTGAGGCGGCCGCCGTTTGCTGAATGCAGGCATCCATTCCCGAG
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTGTGTGCTGTGGCCAATCC
 TGATGGATATGTGTATATCAAACTCAAACCGATTATGGAGGAAGACGCGTCCCAGAAATC
 CTGGAAGCTCCTGCATTTGGTGTCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG
 GGAGCCAGCGACAACCCCTTGCTCCGAAAGTACCATTGGACCCACGCCAATTCGGAAGTGGGA
 GGTGAAATCAGTGGTAGATTTTATCCAAAACATGGGAATTTCAAGGGGCTTCATCGACCTGC
 ACAGCTACTCTCGAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGCCCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCGGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAAATTTGCATTACATTTAGATTGAGATACCGGAGATCCGGAACCTATGGC
 TTCCTCCTGCCAGCTAACAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGCGCATGGCTCTGCTGTCTACATTTAT
 TTGTACCCACACGTGCGAGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCCTGGCGGTGTCCTGCAAGAACTGGTCTGCCAGCCTGTCTCAATTTTGGTCTCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCTCCACCCTGTGGCTGGGGCGGCTGCACATC
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTAGAACCAAGAAGACATC
 TGAGATGATTCTCTACCTCATCCACATCTAGCCAAAGCCAGTGACCTTGTCTGTGGTGCACAT
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCCCTTTAATTTT
 TCGCAGCTCTTCTGGAAAATATTTTCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTTTGGC
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCTCGGGTTCAAGCA
 ATTTCTCCTGCCTCAGCCCTTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCTTGGCTA
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCCGTCCCTCCTTTTTTAGGCCATGAATACAAAGTAGAAGATCACTTTCTCTCAC
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTCCCTTTGTTATTACGTGTG
 ACCAGGATGGCGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATGTCAGGATGGTGAATATCCCCATCTGTCTCAATGGGCTTACCTCCT
 CTTTGGCTTTTGAACCTCACTTCAAAGATCTAGGCCCTCATCTTACAGGTCTCAAACTCACTCAT
 CTGGCTGGATAATCTCACTGGCCCTGGCACATTCCCATTGTGCTGTGGTGTATCTGTGGTT
 TCCTTGTCTCTGGTTTGT
 TCTGTCTATTTGTATCCTGGACCACAAGTTCTTAAGTAGAGCAAGAATTTCATCAACAGCT
 GCCTCTCTTCTTATTTCACTCAGCACGTACCATCTGCTCTTTTGTGTGTGTGTGTGTGTGT
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA
 GCATCTGGTGTGCTTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTQKHGNFKGFI DLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

FIGURE 135

[illegible]

FIGURE 136

MASYLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSK GKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADESGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVVSFNRTFLMMITNKATDGI LFLGKVENPTKS

Signal peptide:

amino acids 1-20

[illegible]

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTSS
GASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAGVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGHAPHRPRWSPNWFWRPVSIIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
 CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
 CTGCTCTGGATGGGCGGCCAGCGATGACCCCATTTGAGAAGGTCATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC
 ATGCCGGAAGGGGAAGTGAGAAGGTTTTCAACGGAAGTTCAGCAACATGGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGCGCTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
 CAACCATGTTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTCCACACTGGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCTAAACTGGCATCCGGCCTTGTGTTGGAGAATAATGTGCGCGTTGTACATCAGCTGAC
 ATGACCTGGAGGGGTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
 GGATTGTGAATAAACTTGATACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFENGLSNMGSGHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCAGGGGCTGCGCGGGGCCGCTGGCAAGGGGACGAGTCAGTGGCACTCCAGGAAGAGCGGC
 CCGCGGGGGGCGATGACCGCTGACCTGACCTGACTCACTCCAGTCTCGGAGCGGGGGGCGCGGAGCTCG
 GGGGCGGACCGCGGGGCGGAGCTGCCCGCTGAGTCCGGCCGAGCCACTGAGCCCGAGCGCGGAGACCGTGC
 GCTCTCTGCTCTCCGAGTCTGCGCACCGCGATGGGCTGAGGAGCTGGCTCGCGGCCATGGGGGCGGCTCGCG
 CTTCCGGCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTGCTGCGCCGCGGCTCCGAGCTGGGCGCTCAGC
 CCCCGGATCAGCCTGCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGCAAGTGAACACATCTCCAACTAC
 ACAGGCTTTCTGCTGAGCAGGATGGCAGGACCTGTCAAACATACATCAAGATCTCTCGCTGCGCTCAGCGGAGTCAC
 AACCTCAGCTTCCTGCGAGCGGGGATACAGGAGCTGCTTTGGGCTGAGACGCGAGAGAAGAACACAGCTGC
 AGCTTCAAGGGCAAGGACCCACAGCGGACTGTCAAACATACATCAAGATCTCTCGCTGCGCTCAGCGGAGTCAC
 CTGTTCACTGTGGCACAGCAGCTTTCAGCCCATGTGTACCTACATCAACATGGAGAATTCACCTGGCAAGG
 GACGAGAAGGGGAATGTCTCTCGGAAGATGGCAAGGGCGTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGCCATCTCGCGGAGC
 CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGGCTCAGCGTAC
 ATTCCTGAGAGCCTGGGCGAGTTGCAAGGCGATGATGACAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
 TTTGAGTTCTTTAGAACCACTTGTGTCCGCTATGCCCCGATCTGCAAGGGCGATGAGGCTGGAGAGCGGGTG
 CTACAGCAGCGCTGGACCTCCTCTCAAGGCCAGCTGCTGTGCTCAGCGGCCGACGATGGCTTCCCTTCAAC
 GTGCTCGAGGATGCTTTCAGCTGAGCCCGACGCCAGGACTGGCTGACACCTTTTCTATGGGGTCTTCACT
 TCCAGTGCACAGGGGAATCAGAAAGGCTCTGCCGTCTGTGCTCTTCAAAATGAAGATGTGCAGAGAGTCTTC
 AGCGGCTCTACAAGGCTGACCTGACCTGAGACACAGCTGTTGACACGCTGACCCGCGGCCACACCGCCG
 CTTGAGAGCTGCATCACCACAGCTGCCCGGAAAGAAAGATCAACTCTACCTCGAGCTCCGACGACCGGCTGCTG
 AACCTCTCAAGGACCACTTCTGATGGACGGCGAGCTCCGAAGCCGATGCTGTGCTGACGCCCGGCTGCTG
 TACCACGCTGGCTGCTACACCGCTCCCTGGCTGCAACCAACCTACGATGTCTCTTCTGGGCACTGCTGGAG
 CGCGGCTCCAAAGCAGTGAAGCTGGGCGCCCGGGTGCACATCTTAGAGAGCTCGAGATCTTCTACGGGA
 CAGCCGCTGCAGATCTGCTCTCGGACACCCACAGGGGCTGCTGTATCGGCTCAGCTCGGGGCTAGTCCAG
 GTGCCATGGCCAACTCGAGCTTACCGGAGCTGTGGGAGTCTGCTCTCGCCCGGACCCCTCATCTGTGCTGG
 AGCGCTCCAGCTGCAAGCAGCTCAGCTCTACAGCTCAGCTGGCCACCGGCGGTGATCAGGAGCATCAG
 GGAGCCAGCGCCAGGAGCTTTGCGAGCGCTTTCGGTGTGCTCCCGCTTTTGTATCAACAGGGGAGAGGCA
 TGTGACAGTGCAGTCCCTTTCGAGCCACAGCAGTGAACACTTTGGCTGCGGCTCTCTCAACTGGGACCGGA
 CTCTGCTAGCAACGGGGCCCGCTCAATGCTCGGCTTCTGCCAGCTGCTACCGACTGGGAGCTTCTGCTGTG
 GTGGGACCCCAACAGCTGGGGAGTTCCAGTGTGTCTACATAGAGGAGGGCTTCAGCAGCTGTAGTCCAGCTAC
 TGCCACAGAGTGTGGAGGACGGGCTGGCAGACCAACAGATGAGGCTGGCAGTGTACCGCTCATATCAGCACA
 TCGCTGTGAGTGACCAACAGCTGTGGCAAGGCCAGCTGGGGTGCAGACAGTCTTACTGGAAGAGGATCTCTGTTG
 ATGTGACGCTCTTTGTGCTGGCGTGTGCTGCCAGTTTATTCTTGTCTACCGGACCGGGAACAGATGAAA
 GTCTTCTGAAGCAGGGGGAATGTGCCAGCTGCAACCCAGACCTGCCCTGTGGTGTGCTGCCCTGACCGCGC
 CCACTCAACGGCTAGGGGCCCTTAGCACCCCGCTGATCACGAGGTAACAGTCCCTGTCCAGACAGCCCGCCG
 GGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACACTTCTGGAGGTATCCCCAGTG
 TGCCCCGGGCGGGTTCGCTTGGCTCGGAGATCTCGTACTGTGTGTTGAGAGCTGACTTCAGAGAGCGC
 TGCCCTTGGCTTTCAGGGCTGTGAATCTCGGAGAGGCTCACTGGACCTCCCTTCGCTGTGCTCTTCTGGGAAC
 ACAGCGTGTGTCGCCGGCCCTTGGGAGCTTGGAGCAGCTGGCTGCTGCTCTCCAGTCAAGTACGCAAGCTCC
 TACCAACCAAGACCCAAACAGCGCTGGCCAGAGGCTCTGGCCAAATATGGGGGCTGCTTAGGTTGGTGGAA
 CAGTGTCTCTTATGTAACTGAGCCCTTGTTTAAAAAACAATCCAATGTGAAACTAGAATGAGAGGGAAGAG
 ATAGACTGCATGCAGCACACAGCGCTGCTCCAGTCTGACTGGCTCGCTTCTGCTGCAAGCAGGATGTAGTTG
 TTGCTGTGAGACAGAGTTGGAACCTCACCAGTGGGCTCTTCACTTCCAACTATCCGCTGCGACCGGCTGC
 CTGCTCTCACTGAGATTCAGGACCACTTGGGCTGCGTGTGCTGCTGCTGCAAGCAGCGGAGTGTAGTTG
 TTGCTGCGCTGCTCCACCACTCAGGACCAAGAGGCTAGGTTGGCAGTGGGCGCTCACCAGTCTCGGGCTG
 GGACCCAACTCTGGACCTTTCCAGCTGTATCAGGCTGTGGCCACAGAGGACAGCGCGGCTCAGGAGAGA
 TTTCTGCAATGTAGCGCTTTCCCTCAGAATTAGGGAAGAGACTTGGCTGCTGCTTCTCGTGTGTTGGTGA
 GAACCGTGGCTTCCCAACATATCCACCTCGCTCCATCTTGAATCAACACAGGAGAACTCACTGACCC
 CTGCTCTCTCCCGAGTCCCGAGTCACTCTCCATCCCTCACTTCTCTCACTCTAAGGATATCACTAGTCCC
 AGCACAGGGGCCGTAATTTATGTGTTTATACATTTTTTAATAGATGCACCTTATGTCACTTTTAAATAAA
 GTCCTGAAGAACTACTGTTTAAAAAATAAA

FIGURE 142

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
>subunit 1 of 1, 837 aa, 1 stop
>MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPPPTWALSFRISLPLGSEERPFLLRF
EAEHISNYTALLSRDGRITLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVETPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIIEELQIFSSGQ
FVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVS LYQF
QLATRPWIQDIEGASAKDLCSASSVVS PSFVPTGEKPECEVQVQFNTVNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGEFQCWSLEEGFQQLVASCYCEVVEDGVADQ
TDEGGSVPVIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLLFLLYRHRNSM
KVFLKQGECA SVHPKTCFVVLPPETRP LNGLGPPSTPLDHRGYQSLSDSPPGARVFTSESEKR
PLSIQDSFVEVSPVCP RPRVRLGSEIRDSVV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTCGCGCGCGCGCGCGGCTACGAAGAGGACGGGGACAGGCGCGGTGCGAAACCGA
 GCCCAGCCAGCCGCGAGGAGCGCGGCGAGGCGGGACGGGAGCCCGGACTCGTCTGCCCGCGCGCGTCTGTCGCCGTGC
 TGCCCGCCCGCGCTCCCGCGCGGAGCGGAGGAGCGCGGCCCGCTCGCGCGCGAGCGCGCGCTTACGCGCGCGG
 CGGGCATGTCCTCTCTAAAGGGCAGGCGCGCGCGCGGGGCGGGTGTGCGGAACAAGAGCGCGCGCGCGGGG
 CCTTGGCGGCGCTCGGGGGCGCGGATGGGCGCGCGCGCGCGCGCGCGCGCGCGTGCCTCCCGGGCGCGGCTCG
 CGCGCTTASGGCGGGCTGGCTCTCGTGGGCGGGGCGAGGGGCTGAGGGCGCGCGCGAGCTGTGCGGCGCGCGCG
 GCGCGCGCGCGCGCGCGCGCGGAGCGCGCGCGGCGATGGCGCGCGCGCGCGCGCGCGCGCGCGCTGGCTCAGCGTGC
 TGTCTGGGCTCGTCTGGGCTTCGTGCTGGCTCGCGGCTCGTCTGCGCGCGCGCTTCCAGTCTGAAGCAGGCGG
 GCCCAGCGCGCGCGCGCGCGAGGGCTCGGCTCGCGGACGGCGCGGCTTCCAGGGCGCGCGGGCGCGCGG
 CGCATGCGCGCGGGCGCGAGCTCTGGCGCGCGCGCTCGGACCCAGATGGCGGCGCGCGCGACAGGAACCTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGTGGCGCGCTACAGAACATGGTCCAGACAA
 TTCTCTGGGAAGTTCAGTTCTTCTCAAGTGGGGTCTGACACATCTGTACCAATTCAGTAGTGGCCACTACGGG
 GTGTGGACGACTCTACCGCGCGCGAGAAAGTCTCTCATGATGCTCAAGTACATGACGACCACTACTTTGGACA
 AGTATGAATGGTTATGAGAGCATGATGACGTGTACATCAAGAGGAGCGCTCTGGAGAACTTCTCGAGGAGTT
 TGAACAGCAGCGAGCCCTCTTTCTGGGCAGACAGGCTGGGCGACCAAGAAATGGAAATCGGCCCTGG
 AGCCTGGTGAGAACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCGGGAGGTGCTTCGGAAATGGTGGCCG
 ACATTGGCAAGTGTCTCCGGGAGATGTACACACCATGAGGACCTGGAGGTGGGAGGTGTCTCGGAGGCTTG
 CAGGGGTGCGAGTGTCTGGTCTTATGAGATGCGCGAGCTTTTTATGAGAATTACGAGCAGACAAAAAGGSGT
 ACATTAGAGATCTCCATAACGTAATTCACCAAGCTATCACATACACCCCAAAACCCACCTTCCAGCT
 ACAGGCTCCACAGCTACAGTCTGAGCGCGCAAGATATCCGAGCTCGCGCATCGACACATACAGCTGTGACGCGGAA
 TTGTCTCATGAGCAATACAGCAACACAGAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTCTCA
 TGAGGTTTCAGCCCGCGCGAGAGGAGATTCTGGAATGGGACTTTCTGACTGAAAATCTGTGATTTGGGAG
 TTGACGGTCCCGCCCTCGAGAGGAAATGGACTCCGCGCAGAGGAGGAGCTTGGACGACATTTCTGATCGAGCTGA
 TGGAGATGATCAATGGCAACGCGAGACAGAGGGCGCATCTTGTGACTTCAAAGAGCTCATGATCGACCTACCGCG
 GGGTGAACCCCATGTATGGGCTGAGTACATCTGGACCTGTGCTTCTGTACAAAAGACCAAGGGAAGAAA
 TGAACGTCCTCTGTGAGGAGGACGCGCTATTTACAGCAGACTTTCAGCAAAATCAGTTTGTGGAGATGAGGAG
 TSGATGCACAGAGTTGGCCAGAGAAATCAATCAGGAATCTGGATCTTGTCTCTCAAATCCCTGAAAG
 AGCTGTGCCCTTTCAGCTCCCGTGAAGAGTGAAGCAAAAGAACCAAGATAAAAAGATAAACATACGA
 TTCTCTTGCTGGGGGTTTCGACATGTTTGTGAGATTTATGGGAACCTTTGAGAAGAGCTGTCTTATCCCAATC
 AGAAGCTCAAGCTCGTGGTTCTGCTTTTCAATTTCTGACTCCAACTGACAAGGCCAAAGTGAACATGATGA
 GAGATTTACCGCATTAAGTACCTTAAAGCCGACATGCAGATTTGCGTGTCTGAGAGAGTTTCTCAAGAGCCTGG
 CCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTGCGAGCTCGACCTCGTGTTTACTA
 CAGATTTCTTACAGCATGTGAGCAAAATACAGTTCTGGGCGCAACAATATATTTTCAAATCATCTTCCGCGGT
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACACCAATTTTGCTTTACTCAGAAAAATCTGCT
 GGAGAACTATGGTTTGGCATCACGTGATTTATAAGGAGATCTTGTCCGAGTGGTGGCTTTGATGTTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGGACTTTTCAACAAGGTTGTCCAGGCAAGTTTGAAGACGTTTAGGAGCC
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTTCTTTGTATCCCAATCTTGACCCCAACAGTACAAATGT
 GTTTGGGGTCCAAAGCATCGACTATGGGTCCACCCAGCGAGCTGGCTGAGATGTGGCGGAAAAAATGATCCAA
 GTTACAGTAAAGCGCAATAATAATGGCTCAGTGAGGACAGCCTTAATGTCCAGCTTTGCTGAAAAGACGTTTT
 TAATATCATTAATTTATTTTCAAATAATTTTGTATGATCAGTTTGAAGTCCGTATACAAAGGATATATTTAC
 AAGTGCTTTTCTTACATAGGACTCCTTAAAGATTGAGCTTTCTGAACAAGAGGTGATCAGTGTGTCCTTTGAA
 CAGGATTTCTTGTGAACATTTATGACGACGCTGCTTAACCTTGACTTGAATGTACCTTCCACAGATTTCACTTTGT
 TTTAAAAAATGTTTCTTTGAGACCTTTGCTCCAGTCTTATGGCAGAAAGCTGAACTTCTTGCAGAAATGAT
 TATTTTAAACAACACTGTAACTCTGTAATGTTCTGTGTGATGTTTAACTTCTTCAAGATTTCACTTTTGT
 GTTTGTGTTTTTTTATCAATGTTTAAAGCCATTTGATGTTCCAGTTGAAGTATAGGAATGTGATTAATG
 CGGTGTTTATCATGTTCTCAGGAGAGCTTTCCAGGTGTGATCATTTCCCTCATGGTACTCTGCTCAGCATGGC
 CAGGTAGGTTTTTTGTTGTTTTGTTTTGTTTTGTTTTGTTTTGAGACGGGATCTCACTCTGTATCCAGGCTGGAATG
 CAGTGGCAATCTTGGCTCACTTTAACTCCACTTCCCTGGTTCAAGCAATTCCTCGCTTGGCTTCCGAGT
 AGCTGGGATACAGGCACACACCCACAGCCAGTATAGTTTGTATTTTATGAGAGCGGGGTTCACCAT
 GCAAGCCAGCTGGCCAGGTAGTTTAAAGCAAGGGGCGTGAACAAGGACAGTACAGTATGCTGCTGTCTG
 TGTAGTTCAATCGGCTTAATAGACCTGGCATTAATTTCAAGAGCATTGCGATTTCTCTCTTGACCCCTT
 GTTTTAAAGGTAATAATTAATGTTTGAATGACAAGAGTGAATTTACATAAATCTGATGTACACAGACT
 GAAACATACACATACCCCTAATCAAAACGTTGGGAAAAATGATTTGTTTTGTTCTTCTATCCTGTCTG
 TGTATGTTGGCTGGAGATGTTTTTCACTCTTCTATTACTGTTTTGTTTTATCTTGTATCTGAAATCCTTTAA
 TTTATTTAATATCTGTTGTGACAGCTCTGCCATTTCTTGAGTACCTGTAGTAGTTATTTATGTGTATCTGAG
 GAGTGTGTTTAGTCTGTTTTATTGTCAGTAAACCGATCTCCAAGAGTTTCTTTTGGAAACGCTTTTCCCTCTC

FIGURE 143B

TTAATTTTATATTCCITACTGTTTACTAAATATTAAGTGTCTTTGACAATTTGGTGCTCATGIGTTTGGG
GACAAAAGTGAATGAATCTGICATTATACCAGAAAGTTAAATTCICAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAACAGTGATAGACTIGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACCACTGAACAATATTTTCTATTGTACTTTTCGAACCATTTGTCTCATT
ATTCCTGTTTGTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAA

145/249

FIGURE 144

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
>subunit 1 of 1, 802 aa, 1 stop
>MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFSSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLNENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVP HIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFEVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKPEPKDKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
KQTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDDVLFNKVVQAGLKTFRSQEVGVVH
VHHVPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
 TTTCCGGCCTTGAGGTTCCACGCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
 ACGGACGACGCC**TATGA**AGCCCTTAGTCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
 CAAGTTTATAGAGAACCTAGTAGCAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
 ACTTTCCCTACAGGAGGCTTCACACCGGAAAATAGGAAAGAAAAACACACGGAAAGTACCCC
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGTCATGCAGAGGAACCTTATATTG
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCAGCCAGAGAGTTGGAATAAT
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAGATCACCTAAAACGAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTTGATGACATCGAACTGTTATTAAACATGCTGTGTAATTC
 TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAATTTTAAACCTACTTGATATTCCATAACAAAGCTGA
 TTTAAGCAAACTGCATTTTTTACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
 AAAAAATATTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
 ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTGGTTCAAGAAAAA

FIGURE 146

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISSETTTTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSPYVTSYKSPVTTLDK
STGIEISTESEDVSQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSALAAAAEHKLKTMYSQLLPVGRTSNKIDDIE TVINMLCNSRSKL
YEYLDIKCVPPMEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCAACCCCTGCTGTCACTCTGTTTTCATAGTGTGAGATCAACCCACA
 GGAATATCC**AT**GGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
 GTGGCAAGTCACTGGACCGGCAAGTTTGTCCAGGCCTTGGTGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTTCCCTGAGACCAGTGCAGAGGCTATGGAAGTGGCGTCTTTCAGGAATCAG
 TTCCATGCTGTGTGCTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTTAAGGC
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTCCAGATTTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCCTCATTTCCAT
 CGTGGGATATGTTGACGAGGATATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCAGC
 CCACAGCCAAAGTGGAAAGGTCCACAGGACAGGATTTGTCTTCAGACTCCAGAGCAAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAGGGAAAAATCCA
 GCGGAAGTGGACTGGAGAAGAAAGCAGCGACAGGCAGAATTGAGAGACGCCCGGAAACAG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACAATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTCAC
 ATTTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCTACACGAGTAGGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTATAC
 CTGCTGACATGTCAAGTTGAAGGCTTGTGAGACCCATATCCAGCATGCGATGTATGACGA
 GGGAAAGGGGACTCCCATATTTCATATGTCCAGTGTCTGGGGAT**TGA**CACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC
 TGAGGTCTTCTGCCCTGAGCCCTGCAGCAGCGGAGTCACAGCTTCCAGATGAGGGGGAT
 TGGCTGACCTGTGGGAGTCAGAAGCCATGGGTGCCCTGAAGTGGGGAGCGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAACTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTTGCCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTCAGGTTTGAAGGCACAGTGTGTGTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGCTTATTTCCACATTAATTTACTTTTCTCTA
 TACCAAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAGAG
 GAGGTAGGATTTTTCATCTGATTTCTATAAGCCACAGTATACCTGATACCAAAACACGGCAAG
 AAAACAGAGAAGAGGAAAGGAAAACATACAGGTCCATATCCCTCATTAACACAGACAAAAA
 TTCTAAATAAAATTTAAACAATTAACATAAACAATATATTTAAAGATGATATATACTACT
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAAGTGTAATT
 CAGCAGATTAATAAGATAAAAAGAAAACCATAAAAAAAAAAAAAA

FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPPSPWRLASILLGLLCGALC
GVVMGMIIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDVRGKNNVTLS
PNNGYVWLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCA**AATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTTCATTATGTGAGATATAATCAAAGAAGACCTACAA
 TTACTATAGCACATTGTTCATTACAACGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
 TCTCCATTAAAGGGAAGAAATTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAATTGTTCAACTTGTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAAATGCCACATGGCTTGTGAGTGTGCTCACTGTTTTACAACATATAA
 GAACCTTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAATGAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAAACCCTAGAAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGTGGAATAGTGAGCTGGGAGATGAATGTGCCAAACCCAAACAG
 CCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCT**TA**
AGGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGAGAAATTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTTCAGCAAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACAAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
 CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGCCCCCTCAAGACTTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTGGGGCCGGCGGCTGCCTGTGCCC
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTTCCACTACTGG
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTGCTTTGCGTAGTGGCCGCTA
 ACGAGGCCGGGGCAAGCCGCTGCCCCAGGCTGGAGGAGAGGGCCCTCGAGGGGGCCGACATC
 CCTGCCCTTCGGGCCTTGACCGCCTTGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC
 GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCCGAGCCGCAGGGGGCGCT**TGA**
 AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCACTGGGGCGCTCAGCCCTGGCCCCCG
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTGTTAGGTCCGGTACTT
 GCGCTTTGTTTCTGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTTTA
 ACGGCCAGATAATAATAATGTAACTTTGCGGTTAAAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLC PGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAAGVGTALALLSCAALVWHFCLRDRWGCPRRRAARAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGGAAAGAGAGCGTCCAGCTGAAGCCAACTCAGCCCTCCGGCTCTCCGGAAGAAAGTTCC
CTGCCCCGATGAGCCCCCGCGTGCCTCCCGACTATCCCAAGCGCGGTGGGGACCGGGG
CCACGCGCGAGCATCGTGCCTGTTTGCCTTGGGAGTAGGATGTGGTGAAGAGATGGGCG
TTCTCCCTTACGGGGCTCACAATGCGGCAGAGAAGATTCGTTGAAGTGTCTGCGCTGCCTGCT
CTACGGCTCTCAATCTGCTCTTTTGGTTAATGTCATCAGTGTGTGGCAGTTTCTGCTTGGTA
TGAGGGACTACCTAAATAATGTTCTCACTTTAAGTCAGAAACAGGGTAGAGGAAGCATG
ATTTTGTACCTACTTTCTGTGTTCTACCTCGGTGATGATGCTGTTTCTGCTTTCTTCTATCA
TGTGGGGATGTGTAGGATATTGTGAACGCTGTGAAGAAATCTGTTGCTTTCTGCATGGTACT
TGTGAAGTTTGTCTTGTCAATTTCTGTGTAGAACCTGGCTTGTGGCGTTTGGACATATGAACAG
GAACTTATGTGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAGAGCCAGGATGACAAATTA
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTAAGT
GCTGTGGAGTAGTATATTTTCACTGACTGTTTGGAAATCAGACAGATGGACTGGCCCCAGAT
TCTCTGCTGTGTTAGAGAATTCAGAGATGTTTCAAAACAGGCCCCACAGAGATCTCAGTGA
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAAACAACATGC
AGGTTGTCAGGGTTTCTGGGAATCTCCATCGGTTGAGCAACAATCTCGGCATGATTTCTCAC
ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGAGCGCTGGGACAGACCAAAATGATGTC
CTTGAAGAGATCAACAACCTCAGCAGCTGTCAATGTCCCTCAGTGAAGACTGTTGAACCAAGCG
TGTCAGAATCTTTGAACCAACATCCATGGCAACAGCTTTAATACACACTTTTGAGATGGAG
GAGTTATGAAGAAAGAAATGTCACAGAAGAAACCAACAACCTTTATTTAGGACTTGTGAAT
TTTGAGTACATACATGTGTTTCAAGAAATGTGAAGAAATAAATGTGCCATAAAATAACA
CCTAAGCATATACTATCTATGCTTTAAATAGGAGTGAAGAAAGTTTCATGTTAAATGAC
CACCTGGACAATTAATTCAGTCCCTTAAATGCTTGAAGACAGATGTATACCCACTGTGTAGC
CTGTGTTGACTTTTACTGAACACAGTTATGTTTGGGCGAGCATGGTTTGTATGACTTTTC
CGCATCCATGCAACAGAGTCACATATGTTGGGACTGGAGCATATGAAGGTTGATTTACTT
CTACCAACTAGTATATAAAGTACTAATTAATGTGTAACATAGGAAGTTAGAAAATCTAATA
ACTTTTATTACTCAGCGATCTATTCCTCTGATGTAATAAATAATATATACAGAAACCTTC
AATATTGGTGACTACCTAAATGTGATTTTGTCTGGTTACTAAAATATTCCTACCACCTTAAA
GAGCAAGCTAACACATTTGCTTAAGCTCATCAGGGATTTTTTGTATATAAGTCTGTGTTTAA
TCTGTATAATCAGTCGATTTTCAGTTCTGATAAATGTTAAGAAATAACCATATGAAAGAGAA
ATTTGTCCTGTATAGCATTAATTTTGGCCCTTCTGCTGTTAATAAGCTTTTACTATTCGT
CCTGGGCTTATATATACATATAACTGTTATTTAAATCTTAACCATTAATTTGAAAATTA
CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGAGAGTTAATAA
GAAATTTTGCACATAACTTAGTTGATTCAGAAAGGACTGTGATGCTGTTTTCTCCCAATG
AAGACTCTTTTGAACATAAACACTTTTTTAAAGACTTATCTTGGCTTCTCCAAACAGAA
GCAATGATCTCCAAGTCAATATAAATCTACAGAAAATAGTGTCTCTTTCTCCAGAAAAT
CTGTGTGAGAATCATTAATAACATGTGACAATTTAGAGATCTTTGTTTTATTCTCACTGATTA
ATATACTGTGGCAAAATTAACAGATTATTAATTTTTTACAGAGTATAGTATATTTTATTT
GAAATGGGAAAGTGCAATTTCTGATTTTGTGTAATTTGTTTTTCTCAGAATATGGAA
AGAAAATTAATGTGTCATAAATATTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWVTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
 TGCCTCGGGCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
 CCCCAGGGGCTGCAGTGGCAGTCCGCCTCTCCAAGGACCAGTCCACACTGCAGGTGCTGG
 ACTCGGCCACAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 TGTGTTGTAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCCTGTC
 TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCGTC
 GTGGTGGGTGGGGAGGAGCCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGA
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCCACT
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAA
 AGACAATGACATCGCCCTCATGAAGTGCAGTTCCTCACTACTTTCTCAGGCACAGTCAGGC
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCAACGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTCAGTGTCTGGGAGCCGCTTCCTTCTCTG
 CCTGCCCCACCTGGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC
 CTCTGCCCCACAGCCTCAGCATTCTTGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACC
 TCGCAGGCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGAGCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGTCTGCGCCAGCCCTGTCCGTCTTCAACCATCCCCAAGCCTA
 CTAGAGCAAGAAACAGTGTGAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTGTCTATTGTTATTACAGCTATGGCCACTATTATTAAGAGCTGTGTAACATCT
 CTGGCAAAAAAAAAA

FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALSLASIIIVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLFFFD
EELTPATPLWIIIGWFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCACTGAGAGACCGAAAGCCTGGCATTCCAGAGGGAGGGAACGCAGCGGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGTGGCTGAGCAATGGCCCTCCAGCCCTGGGCTGGACCCCTGGAGGCTCTGGGCC
 TTTTCTCTTCCAACCTGCTTCAGCTGCTGTGCCGACGACAGCCGGGGGGAGGCGGGCAGGGGCCCATGCCA
 GGGTCAGATACATGACAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAAGAGGCGCTCCAGGATTTTGACA
 CTCTGCTCTGAGTGGTGTATGGAATACTCTCTACGTGGGGCTCGAGAAGGCCATTCTGGCCCTGGATATCCAGG
 ATCCAGGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
 AGAAGAAGAGCAATGAGACACAGTGTTCACCTCATCCGTGTCCGTGTTTCTTACAAATGTACCCATCTCTACA
 CCTGGGCGACCTTCGCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCCGG
 AGGACAAGGTCTGAGGGGAAAGGCCAAAGCCCTTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTTCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCAGC
 CTGTCTCAAGACCGACAACCTTCCTCGCTGGCTGCATCATGACGCTCCTTTTGGCAGCCATCCCTTCGACCC
 AGGTGCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGG
 CTAGAGTCTGCAAGAATGACGTGGCGGCGGAAAGCTGCTGCAGAAAGTGGACACCTTCTTGAAGGCCAGC
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCCGCCACGCGCTCTGCTCCCGCGCATTTCTCCCA
 CAGTCCCCACATCTACGAGTCTTACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTCGGTTTGTGCCCT
 TCTCTCTCTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGAATA
 CTTATAGGGCCCTGAGACCAACCCCGGCCAGGCACTGCTCAGTGGGCCCTCTCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTTCTCTGATGGATGAGCAAGTGGTGGGACGCGCTGCTGCTGGCCGAACTCTGGCTGGAGTATA
 CACGGCTTGAGTGGAGACAGCCAGGCGCTTGTATGGGCACAGCCATCTTGTCATGTACCTGGGAACACACAG
 GGTGCTCCACAAGGCTGTGGTAAAGTGGGACAGCAGTGTCTCATCTGGTGAAGAGATTACGCTGTTCCTTGACC
 CTGAACCTTGTGCAACCTGACAGCTGGCCCCACCCAGGCTGCACTGTTTGTAGGCTTCTCAGGAGGTGTCTGGA
 GGGTCCCGGACCGCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTCTTGGCCGGGACCCCACTGTGCGCT
 GGGACCTGAGTCCGAACTGTGCTCCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGAGAGCGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCTTCGGCTCAGAGCCCGCCGAAATCATTA
 AAGAAGTCTGGCTGTCCCCAATCCATCTGGAGCTCCCTTGCCCCACCTGTACGCTTGGCTCTTATTATT
 GGAGTCATGCCCCAGCAGACTCCAGAGGCTCTTCCACTGTCTACAACTGGCTCCCTCTTGGTGTAGTGCAGG
 ATGGAGTTGGGGTCTCTACAGTGTGGGCACTGAGAATGGCTTTTCATACCTCTGATCTCTCTACCTGGGTGG
 ACAGCCAGGACAGACCTTGGCCCTGGATCTGAACTGGCAGGACATCCCCGGGAGCATGTGAAGTCCCGTTGA
 CCAGGCTCAGTGGTGGGCGCCCTGGCTGCCAGCAGTCTTACTGGCCCACTTTGTGACTGTCACTGTCTCT
 TTGCCTTAGTGCTTTAGGAGCCCTCATCATCTCTGTGGCTCCCATTTAGAGCACTCGGGCTCGGGGCAAGG
 TTAGGCTGTGAGACCTGCGCCCTGGGAGAGGCGCCGTTAAGCAGAGAGTCAACACACTCCAGTCTCCCAAGG
 AATGCAGGACCTCTGCCAGTGTATGTGAGCGTGACAACAACTGCCTAGGCACTGAGGTAGCTTAACACTTAGGCA
 CAGGCCGGGCTCGGGTGCAGGCACTTGGCCATGCTGGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAGAGACCACTTTCTCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGATGACACTCAGCAGGGT
 ATGCACAGCACTGTGCTCCCTTCTTGGACTCCCTTACCAAGCACATGAGCTCTTACAGGGTGGGGGCTAC
 CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCTTCACTTCTGGCCATTCAGGCAAGCCTC
 CAGAAACAGTGTTCAGAGAGCCCTAAAAAAGCTGCCTGTCCAGGACCTTATGTAATGAACACCAACATC
 TAAACAATCATATGCTAACATGCCACTCTGGAACTCCACTCTGAAGCTGCGCTTTGACACCAACACTCCCT
 TCTCCAGGGTATGACAGGATCTGTCTCCCTCTGCTTCCCTTACAGTCTGTGACCGCTGACTCCAGGAAGTCT
 TTTCTGAAGTCTGACCACTTCTCTCTTCTGCTTCACTTGGGACAGCTCTGATCCCTCTGCGCTTCAGGCAAGTGG
 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCTAGTGACCCCTTACCTCTCCCGCTCCCTTTCTTCTTGT
 TTTGGGATTGAGAACTGCTTGTGACAGACTGTTATTATTTTATTAATAATAAGGCTTAAAAAA

FIGURE 158

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKGLQ
DFTDLLLSGDNGLYVGAREAILALDIQDPGVPRLNMI PWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKQSPFPDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPIILMRTLGSQPVLKTDNFLRWLHHDSFVAAIPSTQVVYFFFE
ETASEFDDFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFPNVIRHAVLL
PADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAVVSGDSSAHLVEETQLFPDPEFVRNLQLAPTQGA VFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQIIKEVLAVPNSILELPCPHLSALASYWWSHGPAAPVEASTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYVWVDSQDQTLALDPELAGIPREHVKVP LTRVSGGAALAAQQSYWP
HFVTVTVL FALVLSGALIILVASPLRALRARGKVQCETLRPGEKAPLSREQHLQSPKECRT
SASDVDADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

TGGGTCCCTTAGCCGCGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGGCTCCGTAGAAAG
 TGACGATGGCTGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTGCTC
 TCAGAGGCTGCCAAAATCTGTCACATAATCTACAGTAGGTGGAAGCCATATCTACTGATGGA
 CCGGGTTTCTCAGAAATCTTCAGATCAGGCTCATAATGTCCACATGCTTAACCCAAAAGAG
 GTCTCTTTATGCGCAGAAATTTAAAAAGGAGAAAATCATATCAAGTTATCAGTTGGCTGCA
 CCTGAAGATCATCAAAGAGAAATTTAAAAAGAGTTTGTATTTCTTCTGGAAGAAACTTTAGG
 TGGCAGAGGAAAATTTGAAAACCTTATAATGTTCCTTAGAATACCTGGCGTTGCAGTGCAGT
 ATTTTTTAAATGAGAAGGATATCATGGATTCCTTAAAGAAATGAGAATCTGCACATGGTGATA
 GTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC
 CATCTCTTCCACTTCATTCCGCTCTCTTTTGGAAATTTGGGCTACCAATCCCTTGTCTTATGTT
 CAGTATTCGGTTCTCTGCTACTGATCACATGGACTCTGGGCGGAGTGAAGAAATTTCTG
 ATGTTCTTTAGTTTCTGCGAGGAGGCAACAGCAGCATGCAATCTACATTTGACAAACACCATTCAA
 GGAAACATTTACAGAAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGGTTGT
 GGTTCATTAAATCTGACTTTGCTTTGATTTTGTCTGACCTCTGCTTCCAAACATGTTTAT
 GTGGAGGCTGTATGAAAATTCCTATTAACACGATACCAACAGACTTGGAGAACCTTCATGC
 CAAGTTTGGGACTCTGTTTTGCTCTGTGACCTTGGGCTCCATGTTGAACACCTGTCCAGA
 ATCCGGAAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCACTGTTCTCATATGGCCAAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGTGGA
 TCGCTTCTCTCAGATGACCTCTCGGCTACCCAAAGCATCGCTGTGTTGTCAACCCAGCGCG
 GGCACCAATAGCATAATGGAGGCCATCTCAGCATGTTGTCCTGCGCTCCACCGCTCACGCCCCACGA
 GAGACCTAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAGTTTGGTGTCTTCTATCTCAGT
 AAGAAGCTCAAGGCGAGACATGTGCTCTTAAGATGAACAAACATCATGGAAGCAAGAGAT
 ACAAGTCCGCGGCAGTGCTGCGATGTCATCTCGCTCCACCGCTCACGCCCCACGCCAT
 CCGCTGGTGGCTGGATTGACCAGTCTCCAGCAGAGGGGGCGGCGACCTCAAGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTTCGACGTTTTTGTGTTTCTGCTGGGGC
 TCACTCTGGGGACTCTATGGCTTTTGGGAGCGTGTCTGGGCTGCTGTGGTGGCTGCG
 GGGCGCAAAAGTGAAGGAGACATTAAGGCGAGGTGACGCTTGGCGGGTCTGTTTGTGTG
 GCGATGTCACCATTCTTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCTCTC
 TAGTTATCTCTCTGTTTCTTGAAGAAGCAGGAAAATGGCCAAAATCATCTTTCCACTTGC
 TAATTTTGCTACAAATTCATCCTTACTAGCTCTGCTGCCGTGCTAGCAGAATCTTTCAGCTGCT
 CTGTCCTCTTGTGTTGCCATCAGCAAGGGCTATGCTGTGATCTGCTCTGAGTGACTTG
 GACCACCTGACCTCAGATTTCAGGCTTAAATCCACCTTCTTCTCATGCGCTCTCCGAA
 TCACACCTGACTCTTCCAGCCTCGATTCCTCAGACCTAGTCAGCCTCTCTCACTCTGCCCC
 TACTCTCATATGGAATAACATCAAGAAAGACCTTGATATCTTTTCAGTTTCTGTTTT
 TGTTCTCCACATATTTCTCTCAATGCTCAGGAAGCTCCGCTGTGCTGTAGAGTTTCAGGCG
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT
 TCTTGGCTGAGCAGCAATGGAGAGCTGAGGTTCCTCAGATTTCTGTGAAAATTTAAAGTTTACA
 GCGTTATCTCTCCCCAACTCACTAA

FIGURE 160

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQVRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSEFSGLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELEWF
INSDFAFDFARPLLENTVYVGGIMEKPIKPVPPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVWKCQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVVGIPVFGDQFENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYPVQQPWHEQYLFDFVFFLLGLT
LGTLLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTT
 CTCCATCCCCCAGGTCAGCCCTCAGTGCTGTCCATCCAGCAGGGCTACCCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCGGCGGCTTCATCCCTCCCTTCTCTCCCAAAGCCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACCGAGCCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAAGAGGGGCAGA
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCCAAGCCCACTGGC
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTGAGAGCCCTCCTGCTGGAGGGGGAGTGCCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGTCTACAGCTTCGCGTTCCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACAGCTGGCCTGTCTATCTCAGCC
 TTTGCCAATGATCCTGACGTGACCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGA
 CCCTGGGGACCGAGTGCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT
 CAAGTTTCTCTGGCTTCTCTATCTTCCCTCTCTGAGGACCCCAAGTCTTTCAAGCACAAGAAT
 CCAGCCCCTGACAACTTTCTTCTGCCCCCTCTTGGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCCTTCCACCCACCCACCCCAAGTTACC
 CTCCAGCCACCTGCTGCATCTGTTCTGCTGAGCCCTAGGATCAGGGCAAGGTTTGGCA
 AGAAGGAAGATCTGCACTACTTTGCGGCCCTGCTCCTCCGTTCCCCACCCAGCTTCTCT
 GCTCAATGCTGATCAGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGGCCAG
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCCCTGTGAGGAAAAGCCAGCATCAGGATC
 TCAGCCAGCACCCGTGAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGTCTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTTGAACTTTGTCCCTCCACACTCTGACTGCTCCTTCTCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCTCTGAT
 CTGTGCTGTCTTATCTCTCTTAGGCTTCCTATTACCTGGGATTCATGATTCTTCTCTT
 CAGACCCCTCTCTGCCAGTATGCTAAACCTCCCTCTCTCTTCTTCTTCTTCTTCTTCTTCTT
 GGCCAGCCTGGATGAATCTATCAATAAAACAATAGAGAATGGTGGTCACTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAATTAATAA

FIGURE 162

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLEGECIVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

Signal peptide:

amino acids 1-32

FIGURE 163

[illegible]

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGFALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFVLVGVACSAILMYIFCTDCWLIADVLYFTWLVFDWNTPKKGRRS
QWVRNNAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSPITTVVGEFITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKEGLPETEVLEVN

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

GGCGGCGGGGATGGGGGCGGGGGCGCGGGCGCCGCACTCGTGAGGCCCCGACGACAGGEGCGGGCGGGGCCA
GGGCCGAGGAGCGCGCGCGCCAGACGGGGCGCGGAGAGGCAACGCGGGGACGCCCGCGGACGAGCAGGTGGCG
CGGGCTGCGAGCGTGTTCAGCGCGGAAGCCCTGAGGCGAGCTGTTCACCTGCTCTGACTGCTTGTGCTTGA
CGGCTGTCTCAGCAGGGGGCTGCACCGCTCTGTGACAGCGCAATGGCGCTGTGCGCTCTGTGAAGACCA
GTTCTGTCTGCACTGCTGGTCGGCTTTGCTTCTGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCTACTCACTCTGGAGCCA
ACTGTCATGCTGCTGGAGTGTGTGCTCTGCAGGAGTGTACATGTTACGGACACAGGCCAGGTAGAGCGTCTG
TGCGAAGGAGCAGCAGCATCATCTCAACCACAACTTCAGATCGACTTCTCTGTGGTGGACATGTGTA
GCGCTTCGAGTGTCTGGGAGCTCAAGGTCTCTGCTAAGAAAGGACGCTCTCATGTCGCCCTCATCGGCTGAC
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGTGGAAGGCTGAG
GCGCTGTGCGGACTACCCGAGTACATGTGGTTTCTCTGTACTCGAGGGGACGCGCTTCAGCGAGACCAAGCA
CCGCGTTAGCATGAGGTGGCGGCTCTGAAGGGCTTCTGCTCTCAAGTACCACCTGCTGCCGCGGACCAAGG
CTTCAACCCGCACTCAAGTGGCTCGCGGGAGCAGTCAGCAGTGTATGATGTAAACCTGAATTCAGAGAAA
CAAGAACCCTGCTCTCGGGGATCTCTACGGGAGAAGATACGAGCGGACATGTGCGTGAGGAGATTCTCTCT
GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACACGAGAGAGGACGCGTCCA
GGAGATATATAATCAGAAGGGCATGTTTCAGGGGAGCAGTTAAGCCTGCCCGAGGCGGTGGACCTCTCTGAA
CTCTCTGCTCTGGGCGCAACCTATCTCTGCTCTCCCTCTTCAAGTTTGTGCTTGGGCGCTTTCGACGGGATCA
CTCTCGATGCTGACITTTCTGGGTTGTGGGAGCAGTCTCTTGTAGTTGCGCATGTAGAGAAATCGCT
TGAACCTGGGAGTGGAGATTGCAGTGGAGCTGAGATGGCATCACTGTACTCCAGCTAGGCAACAGACAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAAAAAAACCAGAAATCTGGAGTTGAATCTGTAGTTACTGACATGAAAA
ATTCACTAGAGGCTGAACAGCAGATTGTAGCAGGCGACAGAAAAATCAGCAAGCTTGAAGATGTTACCTTGAGATT
TTTCAGGCTAATGAAAAAAGATGAAGGAAAAATTAAAGCACTCAGAGACCCATGTTGCACCTTCACAAATCAA
CATATGCATGATGAGAGTCCAGGAAGGAGGAGGAAGAAGGTCAGAAAGATGGCCACAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA
AATCAAAGTGTCAAATGACAAAGATCTTGAAAGCAGCAAGAGATGACAACTTATCTTGTTCAAAGGATCTTTG
ATCACTTAACAGCTATTTTCTCTCAGAAATCATGGGAGCAGGAGATGTGGGATGAACACTGTTGAAGGCCA
AACCTTCAAGCTGAATTTGACTTTTGACTCTTAGATGTGCTGACTCTTGTCTCAGGAGCACTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTCTCTTGACTGTAGGAAGGCGCTGTCTTAGCGCGGCACTGGC
TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACAGGGTGGATCATTTGGGGTCAGGCTGATCTCAAATCCT
GAGTTTCAGTGATCTGCCGCTCAGCTCCCAAAGTGTGTGCTTGACGCGCTGAGCAGCTGCCCTGGCCGGA
ATTTCTTTTAAAGCTGAATGATGGGGCGAGGACAGTGCATCGCCTGTGATCCCAAGTACGTTGGATTGTA
AACACTGCACCACTGCGTGCCTAATTTTGTATTTTGTAGTAGAGCTGTGTAGCAGGCTGGTCTGCATCTCT
GACCTCAAGTGACCACCTGCCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTTGGCTTGA
GCATCTTGTGATGTGCTTATGGCCATTGTGATATCTCTATCTTTTGGGAAATGTCTGTTCAGTCTCTTTG
CCTTTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT
CAGTGGCAGAGTCTTGCTCAGCTCAGCCTCAGCCTCTGGGCTGAGTGTCTCCCACTCAGCCTCCTCTGT
AGCTGATATTTTGTATTTTGTATTTTGTAGCTGTAGTTTGTATTTTGTGGAGACAGCAATTTACCATGA
TGCCAGGCTGGTCTTGAATCCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGTGGGATTACAGA
CATGAGCCAGCTGCACTGGCAACTCCCAAATTCACACAGACACAAAAACCACTGTATCAAATGGGCA
GAGGGGCGCGGCTGTGGCCCAACTACAGGGAGACTGAAGTGGGAGTGCCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCAGGTTGTGCGACTGCATTCAGCAGCTGGACACAGAGTGAAGACCTGCTCT

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVSGLVINQVQLCTLALWPVSKQLYRRNLNCRSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFVGLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILSPLFSFVLGVFASGSPLLITFLGVGAASFGVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAACTGAAGTACT**ATG**CATCACTCCCTCCAATGTCTGGGGCA
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGTCTTAGCACTGGGGCACTTCTT
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTGGTGGCAGGCAGGCCG
 GCTTACGCCCTGATACGGCCCTGGGTAGAAGGGAAGGAAGATAAACTTTTATACAAATGGG
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
 TTCTCTAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTGTCTTAGGATCAA
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT
 ACATGTGGTGTCTCTTGTCTCTCT**TAAT**GTGGTATGCCATGGGGTCTTTGCACAAGCCT
 TTCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
 CTTGTTTAATGCTCTCATAAGACCATTGTTTCCCTTTTGCAGCACTTGGCACTCAGTTGTA
 TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCAGAAATGCCAGCTCTGAGC
 TCGGTGAGGGTCAAGGGCATTGCTGTGCTGCCAGGTATAGTGCTTACATGTGGTGGGTGCT
 CATGTTTATAGACTAAATGGAGGAGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
 GATGGTGTAGGGCCAGCATTGTAATTACACGTTGACTGTGCTTGTGAATTATCTGGGGA
 TGCAGGTCTGATTAGTAGGCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGCC
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
 TCAAGACTAGCCTGGCCAACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTG
 GGCATGGTGGCAGCATGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
 AACCTGGGAGGCGGAGGTGCACTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC
 AGAGTGAGACTCTATGTCCAAAAA

FIGURE 168

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRIHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGRLRLRPWVRR
EGKINFYTINGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL

Important features of the protein:**Signal peptide:**

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCTACCTAC
 ATTAAATCTGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCCCAACCTGACCTTCACTCTGGAACGAGAACAGAGTTTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTA
 GCTGCGGCTTTC AAGGTGGGCTTGGCCTGGCCGTAGAAGGGATTTGACAAGCCCGAAGATTT
 CATAGGCGATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCGGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCAATTCCTCGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAGGAACCTTGCCCAAATATGGGTGAGAAAGATGGAGGTGTTGGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTGAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCATCACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCCTCCCCCTCCTTCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATGGAGCTGTCCCCAAGACCAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGTGAATTTGAAACCCAAA
 TCCAAACCTAAGAACCAGGTGCATTAGAATCAGTTATTGCCGGGTGTTGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGAGTTCAAGACCAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCCTGATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVMFCSLVTSLYLPNTEDLSLWLWPKPDHLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCCGCGC**ATGA**CCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCCTGCTTCCCCCGAGGACAGCCGCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCCAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCCGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGGAGACCCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
 CCTGAGTTTAAATTGAAAATAAAGTGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCCLLPEDSRLWQYLLSR
MREHPALRSLRLLTLEQPGDSMMTCEQAQLLANLARLIQAKKALDLGTFGTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

FIGURE 174

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDGRG
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRARRRGLGGRKKKKKAPSADSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRREARRRELEARRRREQEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKS AKKPQSSSTEPARKPGQKEKRV
RPEEKQQA KPVKVERTRRKSEGFMSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEKLAGELAGEEAPQEKAEDKPSTDL SAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATATAAATTA
 ACACCATTGAAAGAGACAATGTGTTTTCATCTGGAATGCTAATAAGATGAAGAGCTTAAAGCCAGAGCCAGA
 TTTTTCACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTCCAGTCACTGGCAGCTTTGAAGCA
 AAAATTCCAGAGCTCAGCTAACCTACCAAGAGCTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTCTATC
 AGAAGGAGCTGGATTTTCAAACCTCTTCTCTTAGATGAGGAAGAGGCCAGGCTGCTCTTGGGAGCCAAAGACCAT
 CTTTCTACTCAGTCTGGTGTGACTTAAACAAAAATTTAAGAAGATTATTTGGCTGCTGCAAGAGGACGGGTGGA
 ATTAGTGAATTAGCTGGGAAGATGCCAATACAGAATGTGCAAAATTTATCATCAGAGTACTCAGCCCTATAACAA
 AACTCACATATATGTGTGGGAAGCTGGAGCATTTCATCCAATATGTGGGTATATGTGATCTTGGAGTCTACAAGGA
 GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGCTCTTCGATCCTCAGCAGCC
 TTTTGTCTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCTTGGCAAGATACTGCATT
 CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAAGTGCATTTACAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTTGGAATTTCTCTATACAGACACCTACAATCCAGATGATGATAAAATATATTTCTCTTTCTG
 TGAATCATCTCAAGAAGGCACTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTGTGAAGAATGATGT
 AGGAGGACACAGCAGCCTGATAAACAAGTGGACGACTTTCTTAAGGCCAGACTGATTGCTCAATTCCTGGAAG
 TGATGGGCGAGATACTTACTTTGATGAGCTTCAAGATATTTATTACTCCCCACAAGAGATGAAGAATCTCTGT
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTAAATGGTCCATATGCTCATAAGGAAGTGCAGACCATCGTTGGGTGCAATGATGGGAGAAAT
 TCCCTTATCCAGGGCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAAGTCCACCGAGATTTCCTAGA
 TGATGTCACTAATCTTATAAGCGGCAGCTCTGTGATGATATAAGTCCGATACCCAGTTCAGAGGAGACCAAGCTT
 CAAAGAGATCAATGTGATTATACAGACTGACACAGATAGTGGTGGATCATGTCTATCCAGAAGATGGCCAGTACGA
 TGTAATGTTTCTTGGACAGACATTTGGAACCTGTCTCAAAGTTGTGAGCATTCAAAGAAAGTGGAAATATGGA
 AGAGCTAGTGTGGAGAGATGTCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTTGTCTGAAGCA
 GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTCAGCTCTCTTGCACAGATGGCAGACATTATTTGGGAAGC
 TTGGCCAGAGCTGTGCTTCTGGCAGAGCCCTACTGTGCTGGGATGGAATGCAATGCTCTCGATATGCTCTTAC
 TTCTTAAAGAGAGCACTAGACGCTCAAGATGTAAATATGGCAGCCCAATCACCAGTCTGGGACATGCAACAGAC
 CATTAGTTCATGAACTGCTGATGAAAGGTGATTTTTGGCATTTGAATTTAACTCAACCTTTCTGCAATCTATAACC
 TAAATCCCAACAGCACTATTTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGCAGAGGATGGAAGCCGA
 TGAAGGAATCTTCAAAACCGAATATGGGCTACTGATTGGAAGTTTCAGAAAGAGGATTTCTGGGATGTATTACTG
 CAAAGGCCAGGAGCAGCACTTTTCATCCACCATAGTGAAGCTGACTTTGAAATGCTATTGAGATTCAGCAGATGGA
 AAATACCCAGAGGGCGACAGCATGAGGAGGGCGAGGTCAAGGATCTATTGGCTGAGTCCAGGTTGAGATACAAAGA
 CTACATCCAAATCCTTAGCAGCCCAAACTCAGCCTCGACAGTACTGCGAACAGATGTGGCAGCGGAGGAAGCG
 GAGACAGAGAAACAAAGGGGGCCCAAAGTGGGAAGCACATGCGAGGAATGAAGAAAGCAAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGGCCAGCTAGTTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC
 TATAAAAAATGCTTCTGTTTGTATATCCCTATATAGTAATTCATAAATGCTTCCCATGGAGTTTGTGCTAAGG
 CACAGACAAATATCTGAATAAGACAATATGTGATGAATATAAGAAAGGCCAAAAATTCATTTGAACAGATTTT
 CCAAGAACAAATCTTGCACAGCAAAATATAAGAATTTCTTAAAAATAGGGGTTTACAGTTGTAATGTTTATA
 TGTGTTTGAATTTTGAATTTATGTCATGTAATAGTTGAGCTAAGCAAGGCCGGAATTTGATAGTGTATAAAGT
 GCTTTATTCCTCGAATGCTATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATCAT
 CATCTCTTATGAGAAGCAGCTACCTTTGTGGTAGGGAATAAGAGGTGACACAAATTAAGACAACTCCCATATATC
 AACAGAGATTTTCTCAGTGAGCCATCTACTCTGGAGATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTCT
 TGGCCACTGGGTTTAAATTTAGTGTACTACAACATGATTACTGAAGGGCACTAATGTTTCCCCAGGATTTCT
 ATGACTGTGAGGATCAAGAGTTAAGAGTTTACAGAGAGAGTTGGTGTGATTGTGTTTATGAGTATATATCACT
 GCTCTACAGGGACAGATGCTTAATAAATACTTTAATAAGATATGGGAAATATTTAATAAAACAGGAAACAA
 TAATGATGATATGATCTGATGGGAAGGCATGCAGATGGGATTTGTAGAAGCAGAGGAAGACAGAGCACT
 AAATTTCTGCTTTGGGGAATTCATATCCCATGAAAGGAAGAACAAATCACAAATTAAGTGAGAGTGAATGATGA
 TGGAGCTCTTTTCACTAGGGATTAAGTAGCTGCCAATTTGTAATTCATCTGTAAAAAAATCTAGATATAACA
 AACTGCTAGCAAAATCTGAGGAACAAATAAATCTTCTGAAGAAATCATAGGAGAGTAGACATTTTATTTAACC
 AATGATATTTGATATATTTTCTCTCTTTAAAAAATATTTATCATCTCTGATATATTTCTTTTACTGCT
 CTTTATTTCTCTGCTGTATTTGATTTTGTATTATATTTGAGTGAATAGGAGAAACATATATAACACACAGA
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATATTTGTTGAATACAGACAGAGTGTAAATTTTAAAC
 AACGGAAGGGTTAAATTAACCTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAAT
 GTAGTATTTGTTTGAATTTAAACATAAATAAGCCTGCTCATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL
GSSEGLDFQTL LLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRS LGPTHDHHYIRT DISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQ RSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIFYP RP GTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVPYV
AGGPTEFKRINV DYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKNWMEVVLEE
LQIFKHSSII LNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYC AWDGNA
CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERI IKTEYGLLIRSLQKKDSGMYCYCKAQEHTFIHTIVKLT LN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACATGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCACC GCCGGGAGGACAGA
 CAACCTCCAGCTTAAGCTGGGAGCAAGACCTGAAGCTGTTCTTCAGGAGCCTGGTGTATTTCCCCACCCAC
 CTCAGCAGTTTCCAGCAGCAGGAGCTGATCAGGTGTGTCTCTGGAGTGGGGAGCAGAAGCGGTGGCTGGCAAGA
 TGGCCCTTGAGAAAGAGGTTTCAGCCTTGACCAGCCGAGCTGCCCGTGACTACAAAGATCCAGAACCATGGGCATC
 GSGTGTAGGTGGGGGGCAGAGGTGTCATGTGCACCTTTCTGTCTCAGCAAGAAAGATGAGAGAGGGGATCTTTGG
 AGCCATTGAGGGTGTGATGTGAGCTACAGAGGGGAGGGAAGGTATTTAAGGTAAACAGTGTGGCAATAAGTTAA
 GAGCAACAGTTTTTGGAGCTAGACCAGCATAGGTTCAAATTCCTCTCTGTCTCTAGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCTAAAGTAGGGCCAAATAATAGCACCCACCTCAT
 AGGGAAGATTAAATGACATAATGTATGTGATGCACTAGCAAAAGTACCACTCCCATAGATCATGCCCCACAG
 TATTTCCACCACCCCTGTTCTCTGCCTTCCCAACACAGGTACTGCAACAGCATGGAGCAGAGGGCGCAGCAGGCTT
 CAGAGCGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTCCGAGAGAGCATCCGCCGGGCACAGGTGAGCC
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGTCTCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGCGCTCAGTGAGGCTCGCGTGTCCAGAGGGACCTCTCTC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
 CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGTTATTCGCTATCAGGCAGGGCGTGAGGATG
 AGCTGACAATCAGGAGGGTGTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCAGCGCAGGTAGGCTTTGTCCTGAGCGATATTCACACTTCCCGACCTTCCCTCCAGAGACGAGCC
 AAGCAGTGAACAATCCCTGCGGGGACAGGCCACAGCATCTCTGGCAGAGGCCCTGTACAGCTACACCAGGACAGA
 GTGCAGAGGCTGAGCTTCCCTGAGGGGCACTCATCCGTCTGTCTGCCCGGCCCAAGATGAGGTAGATGAGCG
 GCTTCTGGAGGGAGAAATTTGGGGGCCGTGTGGGGTCTTCCCTCCCTGCTGTGGTGGGAAGAGCTGCTTGGCCCC
 CAGGGCCACCTGACTCTCTGACCTGAACAGATGCTGCCCTCCCTGCTCTCCAGCTTCTCCGCCCTGCACT
 CTACCTCTGTGTGGATGGGCCCTCTGCACCTCTCTGCTGGTGGGACAAAGCCCTGGACTTCCCTGGGTTCTGG
 ACATGATGGCAGCTGACTCAGCCCGATGCGTCCACCACTCCCGCGCGCTAAAGCCCGGATCTGGCCACC
 CAGATCCCTCACCCTAGAGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTCAAGCTGTGCAGA
 CACCACATCAATGATCCAGAGCAACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCACCCTCAAGGGT
 GGAACCTTCCGCTTCCCATTTCTAGAGCTGGAAACCCACTCTTTTTCCTCATTTCTATCATCTCTAGGACC
 GGAACCTACTACCTTCTCTCTGTGATGACCTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGCTGGAAACC
 ATCCATCAGGCTCTAGTAGTTCTGGCCACCTCTTCCCACTTGGCTCCATGACCCACCCCTCTGAGTG
 CCAGGGTCACTGGGTTGGGCTGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
 CTGTAATGGTCTGAGCGGATTTATTGACAAATGAATAAAGGGCAGAGGCCAGGCCAGGGCTGGGCCTCTTGTG
 CTAAGAGGGCAGGGGGCTTACGGTGCTATTGCTTTAGGGGCCACACGGGAGGGGCTGCTCCAGCTGCCAC
 GCTCTATCATATGGAGCAGGTGTGGGGAAGCGGGGACGGCAGCTGTGTGAGGCAGGGGAAGGAGAAGAGAC
 TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGTGCTCC
 AGCTGGGGGGCAGTGTCTCAGTGGAGGGGAGGCTTTCACGCCACCCACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCAATGAAGAGAGCTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTCTCAAGCTGTGTCCAGC
 TTTTCCCTGGGCTCCAGGACCTTCCCTACCTCCACCAACCAAGGATTAAGCTCAAGCTGCG
 AGTTTACTCTGGGGTTTCAGGAGCCGAAGGCTTAAATAGTTTAAATAGGTGATGGGAAGATGAGATTACCTCA
 TTTAGGGCTCAGGCAGACTCACTCACATACCTCTCTCTGTGGTAGAGACATGAGAGAAGGGGAGGGG
 TCAACATAGAGAGACCAGAGTGGTCTATCAGTGCCCCACAGAGTAGAGCAATGAAGGCCAGCCAGTGC
 AGTCCCGCTGTGTTTCTACTGGTGTGATCAGAAGTGTCTGGTTCTGCTGCCATTGTGCTATTGCTGCTG
 GCAGCCCTGGGCTTGGGCCCTTCCCTCCGGCCCTCAGTGTGGCTGTGCAAGAGCTCTGGGGTTCCCTTCAAGT
 CAGCAGGGGTTAGGTGCTGTCTGCTGAGTCTCTGACTGGGGGCTGGCTAGGACCTGGGCTGTGGCC
 TCTCAGGGGGAGCCTCTCTCATGGCAGGCATCCTGCTTGGGCTGGCCCTCCCCAGAGCCCTGACCAACCCCTG
 GTGCTGTCCCCACAGAGCCCACTCCTGTCTGTGGGGAGGCATCAGCGTGTGTGTCAGCTCATAGCGCT
 TCTCAATGTGTGTCAACCGGAACCTGGGAGGGAGGGAACACTGGGTTTAGGACCAACACTCAGAGGCTGCTGT
 GCCTCCCTCTGACCCAGGACACTCTGAGTTTGGTGGCTACTTCCCTTGGCTCAAGGTAGGGGAGGCCCTCTC
 AGATTGTGGGGCAGATTGTGTAGCTGACTTCTGCTGGAGCTCCAGTCCAGAGGAAAGAGGCCAAGGCCACTT
 TTGGATCAGGTGCTGATCTAGTGGGCCCTTACCTCAGCCCTCTTCCCTGGAGCACTTGGCCACCTGCCCA
 CAGAGAACAAGTGGTCTCCCTGTCCGGGGCGCTTTTCCCTCTGGAGGCTCCCTGAAGCAAGTGGGAG
 GCCTCTGCTGGCTGCAATGTGGATGCAAGGGGCTGCAAGCCAGTGCAGCTGTGATGATGGAGGGGCTC
 CGTCTGCTGGCTGGAGGTGGCATCCACTGGACAGCAGAGAGGGGAGTGGGGTAACATTTCCATTTCCCT
 TCATGTTTGTCTTACGTTCTTTCAGCATGCTCTTAAACCCAGAGGCCCAATTTCCCAAGCCCACTT
 TTTCTGTCTTTATCTAATAAATCAATATTAAAG

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPETAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPS
FSPAPTSVLDGPPAPVLPDGKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT

FIGURE 179A

CACAGGGAGACCCACAGACATATGCAACGAGAGACAGAGGAGGAAAGACAGAGACAAAGGCACAGCGGAA
 GAGGGACAGACACGGGCAGCAGACAGAAAGCGGCCAGACAGAGCTCTTACAGAGGGAGGCGCCAGAGAGCTCCAGA
 AGACACAGGCACGGGAGAGACAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAGAGCCACAGCTCGG
 GCACCTCTCCCCAAAGGACCTAAGTTTCTCCATTTCCTTTAACGGTCTCAGGCCCTCTGAAAACTTTGCC
 TCTGACCTTGGCAGAGTCCCAAGCCCGCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGGTGTGGAGGACTTGGT
 GCTCCTAGACGGGCTCAGTCCCTCCAGCTGCAGTACCACTGCCATGCTCCAGACAGAGCTCGCATCCGGGAGGGG
 TCTGGCAGGGGCTGGCTGTGGGGAGCCCAACCTGCCCTCTGCTGCCCTGTGGCCGTCTCCTGGCTGTGGTGTG
 GCTGCTTCTGCTACTGCTGGCTCTCTCTGCTGCCCTACGCCGGCTGGCCAGCCCTCCCGCGGGAGGAGAT
 CGTGTCTCCAGAGAGCTCAACGGCAGCGTCTGCTGCCCTGGCTGGGCGCCCTCGCAGGCTGTTGTGGCGCTTGA
 GGCTTTGGGAGAGCGTGTCTACTAGAGCTGGAGCAGGACTCGGTGTGCAGCTCGAGGGGCTGACAGTGCAGTA
 CCTGGGCGAGCGCTGAGCTGCTGGGTGGAGCAGAGCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTCTGCAGCTGGGATGGGGAGGCCCTGTAGGCGTGTACAAATACGGGGGGCTGAAGTCCA
 CTTCCAGCCCTGGAGGGGAGGCACCCCTAATCTCTGCTGGGGAGCTGGGGCTCACATCCTACGCCGGAAGAGTCC
 TGGCAGCGGTCAAGGTCCCATGTGCAACGCTCAAGGCTCTCTTGAAGAGCCCGAGCCCGAGACCCGGAAGAGCCAA
 GCGCTTTGCTTCACTGAGTAGATTTTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCAATCCACGGTGC
 GGGGCTAAAGCGCTACCTGCTAACAGTGTGGCAGCAGCAGCCAAAGCCCTCAAGCACCAGCAATCCGCAATCC
 TGTCAAGCTTGGTGGTGAAGCTGGCTAGTATCTGGGGTCAAGGCGAGGAGGGGCCCAAGTGGGGCCAGTGTCTGC
 CACAGCCTTGGCAGCTTCTGTGCTGTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
 CAGAGCAATTTGTTTACCCGTGAGGACTGTGTGGAGTCTCACTTGCAGACGCTGGGTATGGCTGATGTGGG
 CAGCGCTCTGTGACCGGGCTCGGAGTGTGCCATTTGTGGAGGATGATGGGCTCCAGTCAAGCTTCACTGTCTCA
 TGAACGGGTGATGTTTCAACATGCTCCATGACAACTCAAGCCATGCATCAATTTGAACTGGGCGCTTTGAGCAC
 CTCTCGCCATGTCAAGCCCGCTGTATGGCTCATGTGATCTGAGGAGCCCTGGTCCCCCTGACGAGTCCCCCTGT
 CATCACTGACTTCTGGACATGGTATGGGCACTGTCTTAGACAACACAGAGGCTCAATGCTCATGCTGCCCTGT
 GACTTTCCCTGGCAAGGACTATGATGCTGAGCCGACAGTCCAGCTGACCTTCGGGCGGAGCTACGCGCAATTTGCC
 ACAGCTGCCCGGCCCTGTCTGCCCTCTGTGCTCTGGCCACTCAATGGCCATGCCATGTGGCCAGACAAACA
 CTCGCCCTGGGCGCACTGGCAGACCCCTGGGGCCGACAGGCTGATGGCTGCTGGCTGCGTCCGCTCCAGATGACCA
 GCTCCAGGACTTCAATATTCCACAGCTGGTGGTGGTGGGCTCTTGGGAGCCATGGGTGAGTGTCTCGGAGCTG
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCAGAGGCTGTGCCCGGAATGGTGGCAAGTACTGTGAGGG
 CCGCGCTACCCGCTTCGCTCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCGGCGGAGGAGCA
 GTGTGCTGCTACAAACCAGCCACCGACTCTTCAAGAGCTTCCAGGGCCGCTGGAATGGGTTCTCTCGTACAC
 AGGCGTGCGCCCGCAGGACAGTGCAAACTCACTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC
 ACGGGTGGTAGATGGGACCCCTGTCTCCCGGACAGCTCCTCGGCTGTGTGTCAGGGCCGATGCATCCATGCTGG
 CTGTGATGCATCAITGGCTCCAAGAAGAGTTTGACAAGTGCATGGTGTGCGGAGGGGAGCGTTCTGTTGTGAC
 CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACAACATGTGCTCACTATCCCCGGGGGGCCACCA
 CATTTCTGTCCGGCAGCAGGGAACCCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTTA
 TGGCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGGTACTGCTGGGCGACAGCTTGGCTGTGCTG
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 AGTGGCTGGCAACCCCGAGGACACGCTCCGATACAGCTTTCTGCTGCCCGGCCACCCCTTCAACCGCACG
 CCCCCTCCCCAGGACTGGCTGCACCGAAGAGCAGAGATCTGGAGATCCTTGGCGGGCCCTGGGCGGGGAC
 GAATAACTCACTATCCCGGCTGCCCTTTCTGGGCAACGGGCGCTGGACTAGTCTGGGAGAAAGAGAGAGCTT
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 CAGTTGTATTATTTAGTATTTTATCACTTTTATTAGCAACAGGGAAGGGAAGGAGTACAGTGGTCTGGGGAA
 CCGTACCCCTGACCCCTATAGCCCTCAACCTGCCCTGGGCTAGGAAATCAAGGTTGGTGGTATAGGTATAGTGGTG
 TGTGATGGGTGTGTGTGTGTGTGGAATGTGTGTGCTTATGAGGTACAACTGCTTCTTCTTCTCTCT
 TTCTCGAATTTTATTTTTGGGAAAGAAAGTCAAGGATAGGTTGGGCTTCAAGGAGTGAAGGATTTATCTTT
 TTTTCTTTCTTTCTTTCTTTCTTTTCTTTTGGAGACAGATCTGCTCTGCGCCAGGCTGCGATGCTCAAGT
 CCAACATCTCGGCTCACTGATCTCTCGGCTCCCGGGTTCAAGTATCTCATGCTCAGCCTCTCTGAGTGTGTC
 GGATTACAGGCTCTGCCACACGCCCGAGCTAATTTTTGTTTGTGGAGAGAGTCTGCTGATTTGTC
 ACCAGGGCTGGAATGATTTCACTGCTCACTGCAACCTTCCGCACTCGGGTCCAGCAATTTCTCTGCTCAGGCTCC
 CGAGTAGCTGAGATTTATAGCACTTACCAACCGCCGCTAATTTTGTATTTTAGTAGAGACAGGTTTCACTGT
 CATGTTGGCCAGGCTGGTCTGCAAGCTCTGACCTTAGTGTATCACTCGGCTCTCACTCCCAAGTCTGGGGAT
 ACAGGGCTGAGCCAGCGTCCGTGCCACGCCCACTAATTTTTGTATTTTAGTAGAGACAGGTTTCACTGT
 TGGCCAGGCTGCTCTGAACTCCTGACTCAGGTATGACCTGCCCTCGGCTCCCAAGTCTGGGATTTACAGG
 TGTGAGCCACCAAGCCCGGTACATATTTTTAAATTTGAATTTACTATTATGTATCTCTTTGGAGTCAGACAG

FIGURE 179B

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FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNQSVLPDGSAPARLLCRLQAFGETILLELEQDSGVQVEGLTVQYLGQAPPELLGGAEP
GTYLTGTINGDPESVASLHWDGGLLVGLQYRGAEHLQLPLEGGTPNSAGGPGAHILRRKSP
ASGQGGPMCINVKAPLGSPSPRRRAKRFAASLSRFVETLVVADDKMAAFHAGLKRYYLLTVMAA
AAKAFKHPSIRNPVSLVTVRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILETRQDLCGVSTCDTLGMADVGTVCDFARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNLGPLSTSRHVMAPVMAHVDPPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPKDYDADRQCQLTFGPDSRHCPQLPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFENIPQAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLKFSFPGMDWVPRYTGVAPQDQCK
LTCQARALGYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGRHSIYLAALKLPDGSYALNGEYTL
MPSPTDVVLPQAVSLRYSYGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTQDNLHRRQAILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
 AAGAAAAATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
 AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAATTGATCCTGTG
 ACCAGAACTGAAATATTGAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
 TTAAAGTGATTCTCGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTTCTTAAAAATCCAAAATTTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGTCCCAATAAATGACTATACG
 AAAATGGAATAGAAATTTGATCCCATGCTGGATGAGAGAGGTATTGTGTGATTTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGAGTCATCTGTGCTGTCATCATGCCCTTGTAAGTGGTGGGTGGCCC
 GCATGCTGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
 CTCAGAACTACTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
 AAAAAAAAAAAAAAAAAA

FIGURE 182

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVT RTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKN SKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEI F D P M L D E R G Y C C I Y C R R G N R Y C R R V C E P L L G Y P Y P Y C Y Q G G R V I C R V I M P C N W W V
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGCACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCTCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
 GCGCCTGCGCCGTCTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTTGCCATCCTCGGCGGCACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCTTGCTTTGCCTGTCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCCGCC
 CAGGGCCACCACGACCACTGCAAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTTGATAACAAGTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGC GGATGTGGCTGTTTATGAAAAAAAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLPSGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCCTCAGGAGCGGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCTCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTCACCATCCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTTGGTGCGGCTCTGTTCGTG
 GGCTGGGTGCTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
 CCTGGCACCAGAAGAAACCACTACAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTGT
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAA
 AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTCCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCAAGAAAACCTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTACCAAACCAAGTCATTTTCAGTTTGGGCAACCAAACCTTTCTACTG
 CTGTTGACATCTTCTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTtagTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAGGAAATGAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAAGTTGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCCTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAA
 ACTAATCTTTAA

FIGURE 186

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
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Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCAGTGTGCCTCAGTGG
 AGAGTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG
 CTCTTTCTCCGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCTTTC
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAAGTGCACGGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACCTTCCCATCGCACACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTTGTGTATGTTTTTTAACTTTTACTATAAAGC
 CATGCAAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGCTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTTACGCAGAATGAGATATTAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGTGTTTCAAGCATCTACTCTTTTTATCATTTACTTCAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACTTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
 AGATTAAATGAAGGCTTTAATCAGCATTGTAAGGAAATGAATGGCTTTCGATATGCTG
 TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCCAGAGGCTTTTTTT
 TTCTGTGTATTAAATTAACATTTTTAAAACGCAGATATTTGTCAAGGGGCTTTCATTCA
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAAAATATTTTTGTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTGGTTTTTCATTGTGTTACCAAAAAAACAACA
 ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTGACCATTTCTGTTTAGTTTTACTAAA
 ATCTGTAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA
 AAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTTATA
 TTAATAAATTTGTACATTTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGGLWMNCVRQANIRM
QCKIYDSLALSPDLQAAGRLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

TTCGCGCATGGCCTCTGCCGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGT
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCAGCT
GCCCTCTGTGTATCTGCCCTCCTTGTGGCCTGTTCGGCTTGTCTGGTCTACCTTGTCTGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATCCAAAGGCCCGCTGGTGTACCTCTGGGA
TTGTCTTTGTCTATCTCAGGGGTCTTGACGCTAATCCCGTGTCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAAGCGGGAGCTGGGGGCCCTCCT
CTACTTGGGCTGGCGGCCCTCAGGCCTTTTGGTTGCTGGGTGGGGGCTTGTCTGTCTGCATC
GCCCTCGGGGGGGTCCAGGGGCCACGATTACATGAGCCGCTACTCACATCTGCCCTT
GCCATCTCTCGGGGGGCCCTCTGAGTACCTACCAAGAATTACGTCTGACAGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGT
CGTACCTTTTGTCTCTGCTCTGCTATTTTTCTTTGACTGAGGATATTTAAAATTCA
GAAAACAGGCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAACATATGCGGAGGCTGCTTGTCTGTCTGGCTTTGCAACAAGACAGAC
TGTCCTCCCAAGAGTTCTGTCTGTCTGGGGGCTGGGCTTCCTAGATGTCACTGGACAGCTG
CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCCTCCGTCCTGATAAGACG
CTCACCCCTCAGGGCCAGGTCCACGCTATGTAGACCCCGCCCCACCTCCAACACTGCACC
TTCTGTCCCTGCCCCCTCGTCTCACCCTTTACACTCACATTTTTATCAAATAAGCATG
TTTTGTTAGTGCA

FIGURE 190

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIIRDFYNPLVAEAQKREL GASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGQPSHYMARYSTSAPAI SRGPSEYPTKNYV

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Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC
 TTGCCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
 TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGTCTCTTGTGGCTCTCCCGCTGCCCCGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGAC
 GGCTCTAACGAGAGGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCTCTTCATCCTGAC
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
 AGCGCTGCTGTCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTTTATAAAGTCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
 GAACCTGCTTTATGTCTAGATTACATTGATACGAAAGTTTCAATTTGTACTGGTGGTAGG
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

FIGURE 192

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDfYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRNTTMLSKTSTSYV
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Important features of the protein:**Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCTGCCCCATCA
CATACCTACCAGTTTGTGGTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCAGGCTCTGACTG
AGTTTCTTTCAGTTT**T**ACTGATGTTCTGGGTGGGGACAGAGCCAGATT**CAG**AGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAAACAGTCAATAAAAAAATAATCTCCAGA

FIGURE 194

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
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EHLCTESLKSNGRVQFLHDGSC
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Signal peptide:

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FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCGGCCATGGGCTGCCTCCCCGCGCGGCCTGCTGTCTTGGCCCTGACCGGGCTGGCGTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGAAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAAACAACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYQRHYD
EDSAIGPRSPFYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 197

CGGCTCGAGCCCGCCGGAAGTGTCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
 GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGTGGGTGATGAGGTGAC
 CGTCTTTTCTCGTGCTTGCTGCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
 CCGCTGAGGGCGGGACCCACTGCCCCAGCCGTAGGGACCCCAACGCCATCCCAGCCCAGC
 GCAGCCATGCGAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
 CCCCCGACTCCCCGAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTACAGAGCAG
 GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
 GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCCCGCCGGGTCCGAGCCCCGCCCTCCGGGCTGGAAATCGGCAGCCT
 GCTGCTGCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
 CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCCTGCTCCTCAGTCTCCTG
 GCCTTTGCCATGTACCGCCCG**TAGT**GCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTC
 GGACCTTGCTCCCCGCGCCGCGCGGGAGCTGCTGCCCTGCCAGGCCCGCTCTCCGGCCTG
 CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG
 CCCCCCCCFCGACCGCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
 CTGGGAGTGGGCTCCTCGGGGTCGGGCATCTGCTGTCGCTGCCTCGGCCCCGGGCAGAGCCG
 GGCCGCCCGGGGGCCCTCTTAGTGTTCTGCCGGAGGACCCAGCCGCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
 GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAAGTGTGAAGTTTTAAAAAAAAA
 AAAAAAA

FIGURE 198

MTLIEGVGDEVTVLFVSLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPFPNPPCPPGS
EPGPSGLEIGSLLPLLLLLLLLLLWYCQIQYRFFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC
TCAGCTGCACCTCTCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTGTGGTCAGCAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GGAGGACTTGGATGGGTTTGAAGGTTACTCCTGAGTGACTGCTGTGCCCTGGCTTTTGTGG
AAAGCAAGTTCACATATCAAAGATAAATGAAATGCGGATGGAAGCTTTGACTATGGCCTC
TTCAGATCAACAGCCACTACTGGTGAACAGATTATAAGAGTTACTCGGAAAACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
TTGTGTCCGGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTTGCACTGTTCAAGCCGG
CCACTCTCCTACTGGCTGACAGGATGCCCGCTGAGATGAAACAGGGTGCGGGTGACCCGTGG
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATTCTTCATTCTTCTTCTACTGCCTCCA
CTTCATGTATTATTTCTTCTTCCATTACAACATAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTTCTTGGCTTCTCTCCTTACTCCCATCTGGACCCAGTCCCGTGGTTCCTGTCTGTAT
TTGTAACATGAGGACCACAATAAGAAATCTTTATATTTATCG

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNLLAGIHCARIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCTAGCCCTGCTTGACTGAGAACCCA
 CCAGCTCATCCCAGACCTCATAGCAACCTATTATACAAAGGGGGAAGAAACACCTGAG
 CAGAATGGAATCATTATTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACCTGGGTCCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGCACACGC
 TGTGTGGCAATGTGAGGACAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGCCATG
 CAGACTCCAGTTCCCTCCTGCTGCTCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGT
 TGCACCTCCCCACACACCTTGCACAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCTTGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACCAAGGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
 GGCTGATGAGGAGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCTGGACCCAC
 GTGGCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTTGCCTGGAGGTGGG
 CACCCACTGTGTCTGCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCTCATCTCTGT
 TTTCCATGATGAGGCTGGTCCACTCTCTGCGGACTGTACACAGCATCTCGACACAGTGC
 CCAGGGCCTTCTGGAAGGAGATCATCTCGTGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACGGGGATGTGCTCGTCT
 TCATGGATGCCCACTGCCAGTGCCACCCAGGCTGGCTGGAGCCCTCCTCAGCAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGTGTTGGACTGGAAGCTGGATTTCCTGGGAAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGGAGAGGTGGTGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGCCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGTAGGACACATCTACCAAATCAGGATTCCCAT
 TCCCCCTCGACAGGAGGCCACCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGAACGCTTGACGCTGCAAGAGGAGACTGGGTGTGCGGACATTCCTAGT
 TTTCTGGCTAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGCAGAGGGGACATCTGGGCT
 TGCCCATGGTGTGGCTCCTTGACAGTGACAGCGCGGAGCAACAGTACTGACGACACACAGC
 AGGAAGGAGATTCACTTGGCAGGCCACAGCACTGTGCTTGTACGAGGAGGAGCAGGT
 GATTCTTCAGAACTGCACGGAGGAAGGCCGTGGCCATCCACAGCAGCACTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTTCTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC
 AATAAGATTTGTACCTGCGTGGTGATGGAAGCCGCGCAGAGTGGCGATTGACCA
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTCAAGAGGAAAGAGAATTTTGCCCATC
 AAAATCCAGCTCCAAGTGAAGCTAAAGAGCTTATATTTTATGAAGCTGATCCTTTTGTGT
 CTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGEYESPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFDMAHCECHPGWLEPLLSRIAGDRSRVVS
VIDVIDWKTFOYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSFVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSDHSPLDQEATL
RNRVRIAETWLGSGFKETFYKHSPEAFSLSKAEKPCMERLQLQRRLLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
 TGCCCTCCCACCGCTGCTCAGGGCTCTTCATCCTCCCTCGAACCCACAGCCCGCCAGCC
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCACGTCATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCTCGGGTCCCAAGATACAGTCGGCAAGTCTCTGGCTGGCACTG
 CACCCCCAGCCACCCATCAGGCTTTGAGGAGGGCCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGCTCCACCGTGTCTCAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTTCAGCCCTCATGGGCTCGCAACCCACCCCACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCCTGCGGCCATT
 CTGTTCTGGGGGCCGTGGGGAAGGTGTGGACCCCAAGTCTATGTACAAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCTCAGGGCAGCAAGGTGCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCCCTTCGGGGACTCACTACCCCCACCCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTTGAACGGTGGAGGGCAGGGGCAATGGGATGGGAGGGCAAGAGGGGAAGGCAAC
 TTAGTCTTTCAGAGCTGGGGTGGGGTGCCTCTGGATGGGTATGAGGAGGCAGGCGTGGC
 CTCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAAGTCTCTCTTGGGAGGCACCTTCT
 CTTCTCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTCTGCC
 TCTTTGGTTTTTTTCTCATGCCACCTTGCTAAGACAACCTGCCCCCTTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACCTTCCCTTCTATTTCTGGCCTACCCCTTGGTTCTTGACTGTGCCCTT
 TCCCTCTTCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCGACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA
 GCTGGGGCCACAGGGGGCTCTGGCTCCTGCCCTTGACACACCCCGGAACACTCCCCAGCC
 CCACGGGCAATCCTATCTGCTGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTTGTGCACTCACATGAAAGCCTTGACACACTCACTCCACCTTAC
 AGGCCATTGACACAGCTCCTGCACCCCTCTCCCCGTCCATACCGTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTGCACTCTCTCCTTCCCAATTTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTCTGCACTTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGG
 TGTGCGCGTGTCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCCTG
 GTGCTGTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTTGGGCCCTCATCGGTATGG
 TCTCCTCCCATTTCCACACCATTTTGTCTCTGCTCCTCCCTACTCCAAGATGCCGGCA
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCAAGACTTACCCCAAGCCCA
 CTGCTAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA
 AGGGACTCCCATTTGCCCTTCCCTTCTCCTACAGTCCCTTTTGTCTGTCTGTCTGGCTG
 TCTGTGTGTGGCCATTCTCTGGACTTCAAGCCCCCTGAGCCAGTCTCCCTTCCAGCT
 CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGAGTCACTGTTCAAGGCC
 ATCGGGAGCTCTGCCCTCAAGTCTACCCCTTCCCTTCCCGGACTCCCTCCTGTCCCCCTCTT
 CCTCCCTCCTTCCCTTCACTCCTCTCTCTTTGCTTCCCTGCCCTTCCCTTCCAGGT
 CTTCCTCCTTCTCACTGGTTTTTCCACCTTCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT
 GTGATATATATTTTATTATCTCTTTCTTCTTGTGGTGCATCTTGAATTACTGTG
 GGATGTAAGTTTCAAAATTTTCAATAAAGCCTTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGFAASFQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGFAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGSLPIEAI IYLDQGSPEMN
STINIHR TSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSR I I I I I EELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATG**G
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCGGCCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGCCGCGCGCGGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGGAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGC**ATGG**CCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGCCCCA
CGGCTGTCTGCATGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCTGTGGTGGGTGGGCGACATCCCCGTGTGACGGGCGCTGCTCACCAGCTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCGAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC**TAA**GTAGCCC
CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATAAAAAACAGGCCGAT
CGACTGTACGACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG
ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCAGGGCTCTCCTTGGAGGGGGCTCCCCGCTTCCAC
CTGGCTGTATCGGGTAGGGCGGGGCGTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGT
CCACAGGTCTCGGCGCAGTGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAAC
TGGCACAAGTAAGTCCCTCCTCAAACACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCCTAGAGGGGCTCCCGA
GGAGGTGAACCTCAACCAGCTCTGCGCAGGAGCGGCTGCAGTCTTTTCTCCCTCAAAG
GTCTCCGACCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCATAGGGTCTGGTTCC
ACCCATCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAGGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCCGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACAGCGTGCCGCGGCCCTGCACACCTTCGGACATCCAGGC
ACGAGGTGTGCTGGATGTGGCCACACATAGGACCACACGTCACAGCTGGGAGGAGAGGCCT
GGGGCCCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGACGCTGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCTGCCAGGGCAAC
GTGGGGCGGAGACTCAGCTGGACAGCCCCGCTGTGCTGCTGAGCTGGGCTGCTGCTGC
CTCAGGACCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGTGGGCTGTGCGCAGCATACGCGCTGGGCAGGTCCGACAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER
HLAPGSWGGGQLSREGPSLAFEGSMPSPRGDLF

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACAAATGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATTGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCATACTCCA
 TAGCATGGTGCAAAATTTCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTATTCAACAGCG
 TAATTCAGATTCATCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAATAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTTGACTTCTCTTGGAACTACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACCACACACACACGCGTGCACACACGACGACGCGTGCACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGCTCTTAAAAATCTCGTTTTCTC
 TTCTTCTCTTTTAAATTTTCATATCTCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCTTGCTCTTTTAAGGTTACCTAAGGTT
 TGAAACTCTACCTCTTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAAATAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSFQISTDSEVLTHYNITGNTICLFRILDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVVEHVQNF
CDGFLSGKLLKENRESEKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

GCGAGAGCGCGCGCTGGGACCGGAGTGGGGAGCGCGCGTGGAGGTGCCACCCGGCGCGGGT
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGAGCCGGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGCGTGTGGTGGTGGTGGCGGCGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCGAAAAGAAATCTTCGTGGCAA
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTGGACC
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC
 CCAAGGGCAAGGTACCTTGGGAATTATCCACCATTAAAGACAGAATACAGTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAAATATGCAGTTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCTGAGAAAAAGAGAATTTGCCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
 TCTGGTCTCCTAGGCTCTCACTCTGCTCATCAGCATGAGTGTCTGGCTCTCCTATAGTAAGGAA
 AACCTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACATTAAAGAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
 AGGGCCCAGTCTATATATGCACAGTTAGACCCTCCGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC
 CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
 ACAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGTCATGA
 TGAAAGATGGTATGATTCTACATATGTACCATTTGCTCTGCTGTTTTTGTACTTCTTTTC
 AGGTCATTTACAATTGGGAGATTTAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG
 CCTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAACTCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTGAAGTTTTTCTCACT
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
 AAATGTGTCATATCAATTTCTGGATTCAATATAGCAAGATTAGCAAAGGATAAATGCCGAAG
 GTCATCTTCACTTCGAGACAGATTGGATCAATATGATTAAAGTAGAAATCCAAGCTTTGCTT
 GAGAACTTTTGTAACTGGAGAGTAAAAAGATACGGTTTTTA

FIGURE 212

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGGCTTGGCCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCGCGGCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGACAGCCCCGGC
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACC GTTACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
 TGAAGAGATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTGAAAATTC AATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTCAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAATTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
 GTTTTATAAAGTAAAAAA

FIGURE 214

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQ RAGLPPLGHGWGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLT TVQEENEPEVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCCGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCTGTGGCAGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGACGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCTGTACCGGGTCCGGATCCCAAGGCACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTTCGGACCACTGACCCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCAAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCGTCCTGTTCTCATGATGTGAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTTAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTGTCACTTGATACGTTATTTCAGAAACCCAG
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCAGATCGACACGCAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCGGGGCGTCCCGCAGACCGGGGAGCAGGTCTCGGGGGCCACC
ATGCTGGTGA CTGCTACCTTGTCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC T
 GTCAAGATGCCGGGTAAACCCCTGGAAGGGCTGCAGCAATCCCTCCTTCCGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTA CTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCCCTCTACAGTCCCTTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGCTCTTCTCCTGACTTACTCACTATGCTGCTTAACCAA CTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCTTGGCCCTTCGAAACTGGGGGGAGA ACTATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGT CATCTTCATCTTTGCTTCTCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGTGCTCATCGTGTCTTCTCTCTTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGTCCGGTGGAGTCCCTCATAGCCTTTCTACTTATTGAGT
 TGGCTTGTGGATTATAC TTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCTTAGGGCT
 CCTTGTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACAGCATTTGCTCTG
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTCAACCGTGGTAAGGCATGATGCT
 GAGCTGCGGGTACCTTCACTACTGAGGAGCCCTATGCCCTGAGCTGT**TAA**CCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT
 GACTGACTTTGTGACTGTCCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCCATTTAGAAA
 ATAACACACTTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
 VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSTRCAGGLRCLLSDRR
 VLLLTGIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
 PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
 EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFSCSAVMVMALLAVVGLFTVVRHDA
 ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
 314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGCGGGGCGGCGAGAGGAAACGCGGCGCGGGGCCGGGCCCTGGAG**ATC**
 GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGG**TAGA**AGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTTGCTACTTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCAGG
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
 GAACCCGAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
 AGTGGTTTAAAGAGCTGGTGGTTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNQFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGA
 TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
 ACTGGGAAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCAGTGGGACTAGGTGGCAG
 AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC
 TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
 TTATCTCAACGCTATTGTTTAAATGGCTGTGTTTAAATGTGATCTATCTGGAAATGAGGACTC
 CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSIHCMDSLQRYCLMAVFNVYILENEDSE
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCAGTACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTACCCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFRLGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYANSFPVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACCTGGGTGCTCATCAGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTTAGGATCCAGTT
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
 TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
 CCCAAGGGGTCCAATTCTTTCTTCTGGGTGTGAGCGACCTGACTCACTACAGTCGAGCTG
 ACAGGGGCTGTATGCAACTGGCCCTTAAGCCAAAGCAAAAGACTTCAAGGACGACCTTTGAA
 CAATACAAAAGGATGCGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGCTCCCTTCGCTATAACAGCCTTCAAAAACCTTAAGTATAAT
 CAATTTAAAGGGCTCAACCACTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAATCTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGTATAG
 GACAGACCATGTCTTGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCGGAATCTGCAGCGCTCAACCTGGA
 TTCCAACAAGCTCACATTATTTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAACCTGGCTG
 AAAAGTTTTAAAGGCTCAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
 TGCTCGTCATCCTGTGTTATCTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAG
 CTGACGACGCGCTCCCTCATGCAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCCGACCAAGGAATTTTATGTAGATTATAAACCCACCAACAGGAGACCGAGAGA
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAATCGGGCTCCAGGAGTGTGAGGTA
 TGAACCATTTGTGATAAAAGAGCTCTTAAAGCTGGGAAATAAAGTGGTGCTTTATGAACT
 TGGTGACTATCAAGGGAAACGCGATGCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTTGTGCGTTTTAGTGCATTATAATACTGGTCATTTCCTCTCATACATA
 ATCAACCCATTGAAATTTAAATACCAACATCAATGTGAAGCTTGAACCTCCGGTTTAAATATA
 TACCTATTGTATAAGACCTTTACTGATTCCATTAAATGTCGCAATTTGTTTAAAGATAAACT
 TCTTTCATAGGTAATAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLKLSLHLRSNSLRTIPVRIQDCRNLELL
DLGYNRIRSLARNVVFAGMIRLKLHLHFNQFSKLNALFPRLVSLQNLQYQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCPVNLQRLNLDNSNKLTFIQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPLPPTVGATEPGPETDADAEHISFHKKIAGSVALFLSVLVI
LLVIYVSWKRYPAASKQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCTATCCTAAGTTGACTGTCCTT
 TAAAT**ATG**TCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTTGCCGCTATTCCAGTTGGTGTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCTTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTGTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
 ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTTTGGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTCAGTGTGGAAATGTCCAGAGATCTATTCATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAAATGGATGTTGGAATAATTTTGGTCATGGAGATG
 TTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCITCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTTCAGTGTACAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRITMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTA
 GCTCTCGCTCGGTCGCCCGGGCTCAGAAGCTCCGTGGCGGCGCGACCCGTGACGAGAAGCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCCTCTTCAAACCTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGTTACCATTTTTCAGTCAAGTCTGTTTGTGTGCTTCTCAGAAATGTTTTTTA
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAAAGA
 ACACAGTGGATGTGCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGTGAATGGCTCAGCAGCCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAAATAAAAAGAACGAATGTCTCGGCCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATATTTGCTGGCTTAGGAC
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAC
 TCTAATTTCTGCATATAAAAAATTTTAAAGTTATTTGTTTGCCTTCAGGCCAAGTCTGTTCAATG
 CTGTACTATTGCTTAAAGAGAATTTGGTAACTTGGTTGATGTGTTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTTC
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGACAAGTGAAGAATGTTTAA
 TCATTCTGTCATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAATGTG
 CTTATTGTAATAATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA
 AGGTTAATTATTGTATATTTTAAAAATTACACTATAAGAGTATAATCTTGAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCAATTAATAAGTT
 GTAAACTCTAATCTTATACTTTATTGAAGAATAAAAGATATTTTATGATGAGAGTAAACAATA
 AAGTATTCATGATTTTTCACATACATGAATGTTTCATTTAAAGTTTAACTCTTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTTAATTTTGTCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA
 GGTACTTTTGTGCTGCATTAATTTGCTTGAAAGTGTTAAACATTATATTATATAAAGGTATC
 CTTTATGAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
 TTAAAAATAAGAACATTTAAAAATATAAATCTAGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCCCTAATCTTGGGTAACTTAGTATATAAACAAATTTACTTTTAT
 TTAATTTCCCTTGTAGCAAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
 CTCATATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTTAGCATATATAGCAATTTAGATAT
 TGTATTGTTGCTCATTTATAATATGCTACCATGTAGCAATAATTAACAATTTTTATTAAAA
 TAAATATGTGAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTTCTCTCTCTGTA
 CTGTCACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

FIGURE 231

CGCGGCGGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAAACCGGCCATGCT
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCTGACTCGG
 GTGGATTGTAGCGGCTGGGCCCCACATCATGCCGGTGGCCATCCCTCTGGACACAGCCCA
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCGGGGCT
 ACACGACGTTGGTGGCTGGATCTCAGCCACAACCTGCTCACCAGCATTCACCCATGCC
 TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCTGCC
 AGCCGAGAGCTTCACAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC
 CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCACTT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCGGTGCCAACCTCCGAGACTTGCCCC
 TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCATTGGTCCGGGTGCCTTCGCGGGG
 CTGGGAGGCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCGCTGAGCTACCGGGCCTGCAGGTCTCGGGCAACCCCAAGCTTAAT
 GGGCAGGAGCTGAGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC
 AACCTGGTGCCCTGCGCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT
 GGGCCAGGATGTGGCTGCGCGCGCCTGGTGGGGAGGGGCACTACCCCGGAGGCGCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
 ATCTCT**TGA**AAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCTCAG
 GTCCCGAGTAACTTATGTTCAATGTGCCAACACAGTGGGGAGCCCGCAGGCCTATGTGGCA
 GCGTCACCACAGGAGTTGTGGGCTTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTCACCCCTTTGCTACGTTGCTTCCCCAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGTCCCCCTCCTGCTTCCCTTCCCACTTATCCCCCAAGTGCCCTCCCTCAT
 GCCTGGGCGGCTGACCCGAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCCCAGTCACTCAGGGGCGAGTT
 TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
 TTCCCTAGAACTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCTTCTCATGTGAC
 AGATGGGAAACTTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGCAGTGGC
 ATGACTGGAGCACAGCCTCCTGCCTCCCAGCCCGGACCCAAATGCACCTTCTTGCTCCTCTA
 ATAAGCCCCACCCTCCCCGCTGGGCTCCCTTGCTGCCCTTGCCCTGTTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
 GTGCGGCATGGGCTAAGTCACTCTGCCCTCTGGAGCCTCTGGAAGCTTAGGGCACATGGTT
 CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCAGGCATCCAGACTGGAAACCTACC
 CATTGTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
 CTGGCTGGGATCTCCAAGGGCCTCCTGGATTCACTCCCACCTGGCCCTGAGCAGCAGCAGC
 CCTTCTTACCTCCCAAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC
 TCTACCCCCAGGCGAGCATCTCAGCTTCCGAACCTGGGCTGTTTCCCTTAGTCTTCATTTTA
 TAAAGTTGTGCTGCTTTTAAACGGAGTGTCACTTCAACCGGCCCTCCCTACCCCTGCTGGC
 CGGGGTGGAGACATGTCATTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAT
 ATTGTCCTGGCGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATAGTGGCCATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC
 CCATCATCTATCTAACCGGTCTTGATTATAATAACACTATAAAAGGTTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTRPCFPQCCEVETFGLEDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLNSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTFRAGLPAPTI
QSLNLAWNRLHAVPNLRDPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCTGTGGGTCTGAGG
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATTATGCGTCAATCCCCA
 AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCTGT
 GTTCCAGGCCCTTACCTGCTGGGCTAAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTTTCAC
 GGGAGGCTTGGCAGTTTTTCTTACTCTGTGGTCTCCAGATTTAGGCCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTGTCTGCTGCTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGATCTTATTTATGCATTACTTGCTTCTTGCATGAT
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTTGTAATATCTT
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT
 ATTTTTTTACTTGGACATGAAACTTTAAAAAAATTCACAGATTATTTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAGAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGGTTATTCTTTGTATTCACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
 CTTCAGCCAGGAATCTACAGGCCAGCATGTATTTCTACAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGGLTCWALTAEPGWGQNGGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPNRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSLFTIKKDLRLSHAMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGGCTTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGTTG
 TGTTTGGCAAAAGTGAAGATGAGCATTTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACGTACCTAGTGAAGGTTGAGATGCAAAT
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATTTGCGATTTCGTGGTGACATCATGCATTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGAGGCTGGGTACCCAATATACAA
 AGAGCAGCACCTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAAACACTACTTGGT
 ATTGAATACACCACTTGAGGACAATATCATGACTCAGGCTTTATCAAGTTTATGTTCTGGAC
 TGGTAGCTTCATTCTGGGAACACCCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
 TCAAGGTGAAGGATTGATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTT**TAA**

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRLKLEKPLRFRGVHHFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGCGAGGGTTGTGGCGCAGCAGTCTCCTTCTCGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGC
 TTAAGAAGTAAAA**ATG**GCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCT**GA**GATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTATGTTT
 TGAGTTTTGAATAGTTTTATGAAATTCCTTATTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTATTCCTGAGATTTAGAA
 CTGTATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTGT
 CTCTCTGGCTGGGCGCGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
 AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTGAACCCGGGGGCGAGAGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACCTAGCCTGGGGGAGAAAGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA
 AAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRGTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:**Signal peptide:**

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGGCCCGCAACACTCCGCTCTCACCTCTGGGCCCCTGTCATCTAGAGGAGGGCCGCTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT
 GGTCACTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGGAAAGCTGACCCCAAGCCACCTTCACTGGACAG
GATGAGAGTGTCAAGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTATTTCGAAGCTACATGAGCTTCAAGCATGAAAAACCATCCGCTCTGCCACGCTGGCTGGCA
 GCCTCGCCCAACGAAGGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAGAAATTCGGGGGGTGCAGTGGTGTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTGACTTG
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCACAGACAAACAAATACG
 AGGGATGGCCAGAGCTGTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTAGGGTGCC
 TGTGGCTCTTCTCAGCCAGGGGCCCTGAAGAAGCTCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGAAGTGTGTCAGGTCTTGCACGC
 TGTGTGCGCCTCTCCTCCTCGGAAACAGAACCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGTCTTCTGGAACCAGCTGTCTGTGAGAGAATGGGGTGTCTTCTGCAGGG
 ACTGCTGACGGCTGTCTGAGGAAGACAACTGCCAGACTTGAGCCCAATTAAATTTTA
 TTTTTGCTGTTTTGAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLLALIFAIVTTWMFIRSYSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:**Signal peptide:**

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGCTCTGGGGAT
 CCAGAAACCCATGATACCCCTACTGAACACCGAATCCCTTGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTGCTGTCTCTAGTCTCTAGTCTCAAATCCCAGTCCC
 CTGCACCCCTTCTCTGGGACACTATGTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCATCGATATTAGACAGACAGTGT
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTGTCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT
 TCCTTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTACCTCAGCACAAGCCACGACTGAGGCATTAAATCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCTTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA
 TACTGCGGGATCTCTCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
 TATTTGGAATTAAGTTTCTGACTTT

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPAASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFQAGSSYTTGEMLSLGVGILVGCCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

FIGURE 244

MRSTILLFCLLGSTRSLPQLKFPALGLPPTKLAPDQGTLPNQQSNQVFPSSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHHPVLPFI FVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGS LPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG
GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCCTCCGCCCTCCAGCTCCGCGCTGCCCG
GCAGCCGGGAGCCATGCAGACCCAGGGCCCCGCCCTCCCCGCAGCGGCTCCGCGGCTCC
TGCTGCTCTGCTGCTGCAGTGCCTCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCGAGACGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGTTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCCTGAGGAAAAGCTTTGAG
GAGTCTTGGACACCCAACTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT
TGGGAAAATTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATT
AATGGAGCTGAATGTTTCAGGACCTCTCCCATGAAGCTATAATTTATTTGGACCAAGGAAG
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amino acids 1-30

amino acids 195-217